

STIC-Biotech/ChemLib

86502

Fr m: Davis, Minh-Tam
Sent: Tuesday, November 19, 2002 9:55 AM
To: STIC-Biotech/ChemLib
Subject: Search request for 09/878454

Please search in commercial database and in issued patent files:
SEQ ID NO:2, wherein positions 116-128 of SEQ ID NO:2 are mutated.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

muty date

60, 210, 939

CRF 6/2000

of page 2

1. need xxx at 116-128

2. one x at 127

Point of Contact
Susan Hanley
Technical Info. Specialist
CM1 6B05 Tel: 305-4053

TYPE OF SEARCH:

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
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NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN.
CC -1 SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK.
CC -1 TISSUE SPECIFICITY: UBIQUITOUS.
CC -1 SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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CC
CC EMBL: U83236; AAB39758.1; -
CC EMBL: U85611; AAB53387.1; -
CC EMBL: U82226; AAC51106.1; -
CC EMBL: AB021866; BAA36281.1; -
CC EMBL: BC000846; AAB00846.1; -
CC PDB: 1DGV; 08-DEC-99.
CC GeneW: HGNC:16920; CIB1.
CC MIM: 602293; -
CC InterPro: IPR002048; EF-hand.
CC Pfam: PF00036; ehand; 2.
CC ProDom: PD000012; EF-hand; 1.
CC SMART: SM00054; Eph; 2.
CC PROSITE: PS00018; EF-HAND; 2.
CC KAM: KAM00001; Repeat: 3D-structure.
CC FT CA BIND 116 127 EF-HAND 1 (POTENTIAL).
CC FT CA BIND 161 172 EF-HAND 2 (POTENTIAL).
CC FT CONFLICT 44 44 T->S (IN REF. 3 AND 5).
CC SQ SEQUENCE 191 AA; 21717 MW; 9AA6EA789781E55 CRC64;
Query Match 100.0%; Score 962; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 4.3e-70;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 61 LEBLANPKEKICRFVSPAKDSLSFEDFLDLSVFDATPDIKSHYARIFEDDD 120
DB 61 LEBLANPKEKICRFVSPAKDSLSFEDFLDLSVFDATPDIKSHYARIFEDDD 120
QY 121 GTLNREDLSRLVCLTGEEDTRLSASEMKOLIDNLEESDIDROGTINLSEFOHYIRS 180
QY 121 GTLNREDLSRLVCLTGEEDTRLSASEMKOLIDNLEESDIDROGTINLSEFOHYIRS 180
QY 121 GTLNREDLSRLVCLTGEEDTRLSASEMKOLIDNLEESDIDROGTINLSEFOHYIRS 180
QY 181 PDFASSFKIVL 191
DB 181 PDFASSFKIVL 191

RX MEDLINE-99069785; PubMed-9852683;
RA Seki N., Hayashi A., Abe M., Araki R., Fujimori A., Fukumura R.,
RA Hattori A., Kozuma S., Ohira M., Hori T., Saito T.;
RT "Chromosomal assignment of the gene for human DNA-PKcs interacting
RT protein (KIP) on chromosome 15q25.3-q26.1 by somatic hybrid analysis
RT and fluorescence in situ hybridization."
RL J. Hum. Genet. 43:275-277(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE=Fetal kidney;
RX MEDLINE-99160477; PubMed-10051332;
RA Saito T., Seki N., Hattori A., Hayashi A., Abe M., Araki R.,
RA Fujimori A., Fukumura R., Kozuma S., Matsuda Y.;
RT "Structure, expression profile, and chromosomal location of a mouse
RT gene homologous to human DNA-PKcs interacting protein (KIP) gene".
RL Mamm. Genome 10:315-317(1999).
RN (3)
RP SEQUENCE FROM N.A.
RA Naik M.U., Naik U.P.;
RT "Cloning and tissue distribution of murine calcium and integrin
RT binding protein, CIB-1".
RL Submitted (Jul-1999) to the EMBL/Genbank/DBJ databases.
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukuishi Y., Konno H., Aachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakai T., Pesole G., Quackenbush J.,
RA Schriml L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nomberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection".
RN Nature 409:685-690(2001).
CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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CC
CC EMBL: AB006463; BAA74429.1; -
CC EMBL: AB017361; BAA36165.1; -
CC EMBL: AF173010; AAC89860.1; -
CC EMBL: AK010345; BAB26868.1; -
CC HSSP: Q99828; 1DGV.
CC MGD: MGI:1344418; Cbl1.
CC InterPro: IPR002048; EF-hand.
CC Pfam: PF00036; ehand; 2.
CC ProDom: PD000012; EF-hand; 1.

DR SMART: SM00054; EFh: 2.
 DR PROSITE: PS00018; EF_HAND: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127
 FT CA_BIND 161 172
 FT CA_BIND 172
 SO SEQUENCE 191 AA; 21763 MW; C85B603A19F9D9AC CRC64;

Query Match
 Best Local Similarity 94.5%; Score 909; DB 1; Length 191;
 Matches 180; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGSSGRLSKELLAEYODLTFLTKOELLAHRRFCELLPEQORTVSSSLRAQVPEQILS 60
 DB 1 MGSSGRLSKELLAEYODLTFLTKOELLAHRRFCELLPEQORTVSSSLRAQVPEQILS 60
 QY 61 LPELKANPFEKRICRVFSTSPANDSLSFEDFDLDSVFSPTATPDIKSHYAFRIPEFDD 120
 DB 61 LPELKANPFEKRICRVFSTSPANDSLSFEDFDLDSVFSPTATPDIKSHYAFRIPEFDD 120
 QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILESDIDRGTINLSEFOHYSRS 180
 DB 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILESDIDRGTINLSEFOHYSRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 3
 KIP1_RAT
 ID KIP1_RAT STANDARD: PRT: 191 AA.
 AC 09R010;
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs interacting protein) (Kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PKRDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99452760; PubMed=10523297;
 Kauselmann G., Weiler M., Wulfe P., Jessberger S., Konietzko U., Scafield J., Staubli U., Berleiter-Hahn J., Strehardt K., Kuhl D.;
 "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)- and integrin-binding protein and are regulated dynamically with synaptic plasticity.";
 EMBO J. 18:5528-5539(1999).
 CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-ITB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-ITB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC EMBL; AF136585; AAF08368.1; -
 DR HSSP; Q99828; IDGV.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 2.
 DR ProDom; PD000012; EF-hand; 1.
 DR ProDom; PD000012; EF-hand; 1.

DR SMART: SM00054; EFh: 2.
 DR PROSITE: PS00018; EF_HAND: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127
 FT CA_BIND 161 172
 FT CA_BIND 172
 SO SEQUENCE 191 AA; 21800 MW; 3B00B0228879FC7 CRC64;

Query Match
 Best Local Similarity 94.4%; Score 908; DB 1; Length 191;
 Matches 180; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGSSGRLSKELLAEYODLTFLTKOELLAHRRFCELLPEQORTVSSSLRAQVPEQILS 60
 DB 1 MGSSGRLSKELLAEYODLTFLTKOELLAHRRFCELLPEQORTVSSSLRAQVPEQILS 60
 QY 61 LPELKANPFEKRICRVFSTSPANDSLSFEDFDLDSVFSPTATPDIKSHYAFRIPEFDD 120
 DB 61 LPELKANPFEKRICRVFSTSPANDSLSFEDFDLDSVFSPTATPDIKSHYAFRIPEFDD 120
 QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILESDIDRGTINLSEFOHYSRS 180
 DB 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILESDIDRGTINLSEFOHYSRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 4
 KIP2_MOUSE
 ID KIP2_MOUSE STANDARD: PRT: 187 AA.
 AC 09Z309;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Kinase interacting protein 2 (KIP 2).
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99132027; PubMed=9931475;
 Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T., Saito T.;
 "Structure, expression profile and chromosomal location of an isoform of DNA-PKcs interacting protein (KIP) gene.";
 Blochim. Biophys. Acta 1444:143-147(1999).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC EMBL; AB016080; BAA36545.1; -
 DR HSSP; Q99828; IDGV.
 DR InterPro; IPR029293; KIP2.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART: SM00054; EFh: 2.
 DR PROSITE: PS00018; EF_HAND: 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127
 FT CA_BIND 157 168
 FT CA_BIND 168
 SO SEQUENCE 187 AA; 21703 MW; D21D21DCBDB06F5C CRC64;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 17:57:51 ; Search time 31 Seconds

(without alignments)
1269.516 Million cell updates/sec

Title: US-09-878-454a-2

Perfect score: 962
Sequence: 1 MGSGSRLSKELAEYDLET.....EFQHYISRPDPFASSFKIVL 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_podent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvitus:*
16: sp_dactariap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413	42.9	311	5	Q93640
2	369	38.4	185	11	Q9D9N5
3	346	36.0	187	4	Q96077
4	343.5	35.7	206	5	Q9W205
5	277	28.8	54	6	Q9GLJ2
6	227.5	23.6	180	5	Q9GR83
7	206	21.4	175	5	Q9U0X7
8	194	20.2	175	10	Q9LS47
9	193	20.1	175	10	Q93VF2
10	184.5	19.2	169	5	Q9NPN1
11	183.5	19.1	244	5	Q20804
12	182.5	19.0	189	5	Q9VNF9
13	180.5	18.8	170	5	Q9NKK7
14	180.5	18.8	170	5	Q9NKK7
15	177.5	18.5	115	11	Q99LQ9
16	176.5	18.3	187	5	Q9VWX8

17	174	18.1	200	5	Q8SRF8	08srf8 encephalit
18	171.5	17.8	175	3	Q9HDE1	09hde1 cryptococcu
19	171.5	17.8	177	3	Q9HDD3	09hdd3 cryptococcu
20	171	17.8	274	10	Q9AWM4	09awm4 oryza sativ
21	170.5	17.7	195	5	Q23643	023643 caenorhabd
22	170.5	17.7	213	5	Q16343	016343 caenorhabd
23	170.5	17.7	213	10	Q9LTB8	09ltb8 arabidopsi
24	170	17.7	170	4	Q8WYJ4	08wyj4 homo sapien
25	170	17.7	173	4	Q96LZ3	096lz3 homo sapien
26	170	17.7	190	5	Q9NAY9	09nay9 naegleria f
27	165.5	17.2	161	10	Q9AY39	09ay39 oryza sativ
28	164.5	17.1	226	10	Q81446	081446 arabidopsi
29	159	16.5	190	3	Q9EX50	09ex50 magnaporthe
30	159	16.5	190	3	Q9EX50	09ex50 magnaporthe
31	154	16.0	196	5	Q9N2Y1	09n2y1 caenorhabd
32	154	16.0	225	10	Q8W5C8	08w5c8 oryza sativ
33	152.5	15.9	226	10	Q81447	081447 arabidopsi
34	151.5	15.7	246	10	Q82641	082641 arabidopsi
35	151	15.7	246	10	Q81328	081328 arabidopsi
36	148	15.4	192	10	Q81223	081223 arabidopsi
37	148	15.4	192	10	Q9UM19	09um19 homo sapien
38	146	15.2	191	4	Q9U5J0	09u5j0 trichomonas
39	141.5	14.7	153	5	Q9U5J0	09u5j0 trichomonas
40	141.5	14.7	160	5	Q9U5J9	09u5j9 trichomonas
41	141	14.7	220	4	Q9NS60	09ns60 homo sapien
42	141	14.7	220	4	Q9HD11	09hd11 homo sapien
43	141	14.7	220	11	Q9JMG6	09jmg6 rattus norv
44	141	14.7	225	4	Q96K86	096k86 homo sapien
45	141	14.7	252	4	Q9WZ11	09wz11 homo sapien

ALIGNMENTS

RESULT 1

ID Q93640 PRELIMINARY: PRT; 311 AA.

AC Q93640: 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F30A10.1 protein.
GN F30A10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae.
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;

RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9851916;

KA none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology."

RT Science 282:2012-2018(1996).
RL EMBL: 281072; CAB03019.1; .

DR HSSP; Q99828; IDGV.
DR InterPro: IPR02048; EF-hand.
DR Pfam: PF00036; ehand; 3.
DR ProDom: PD000012; EF-hand; 1.
DR SMART: SM00054; Efh; 2.
SQ SEQUENCE 311 AA; 35960 MM; 97AFOAF56AF526F CRC64;

Query Match 42.9%; Score 413; DB 5; Length 311;
Best Local Similarity 42.5%; Pred. No. 1.6e-28;

Matches 88; Conservative 41; Mismatches 52; Indels 26; Gaps 5;

0Y 1 MGSGSRLS-----KELAEYDLETFLTKQELLAHRRFCFLLEQEOFTVSS 48
DB 111 MGNASSLSLEINLFSGKGVFTREQLDEYDQDCTFTFRKDIIRLYKRFVALNPHK--VPTN 167

QY 49 LRAVP-----FEQILSLPELANPKRICKRVSTSPAKDSIFEDFDLILSVFSDTA 102
 Db 168 MGRNRPATITLTFFEEVKEKPELKENPKRICEVFS-EDGRNLSFDFDLMEVSFEEMA 226
 QY 103 TPDLKSHYARIRDEDDGTLNEDLSRYNCLTGEDEDTRLSASEKQILDNILESDI 162
 Db 227 PLQDLKTYARIRYDDELDGHDLSKMRSLTRD-----ELSDVEVEFIERIEEADL 282
 QY 163 DRDGTINLSEFOHYISRSPDFASSEFKI 189
 Db 283 DGDSSINFAFEFHYVSRSPDFIRTFHI 309

RESULT 2

Q9D9N5 PRELIMINARY; PRT; 185 AA.
 AC 09D9N5;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DE 1700041E20R1K protein.
 GN 1700041E20R1K
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shidpara K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito K.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuenli P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hornann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shidpara Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohlsuki S.,
 RA Hayshtzaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK006670; BAB24697.1; -.
 DR HSSP; O99828; IDGV.
 DR MGD; MGI:1920509; 1700041E20R1K.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; ehand; 2.
 DR PRINTS; PR00450; RECOVERIN.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; Eph; 2.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 SQ SEQUENCE 185 AA; 21637 MW; 70C6B3EBF73844CB CRC64;

Query Match 38.4%; Score 369; DB 11; Length 185;
 Best Local Similarity 44.2%; Pred. No. 6.1e-25;
 Matches 80; Conservative 37; Mismatches 50; Indels 14; Gaps 5;

QY 11 ELAAYODITFLTKQELILAHRRFCFLPQEQRTVSSILRAQVPEQILSLPELANPKR 70
 Db 12 EELAEQALTFILRNELICIHDTFLKICSGKHKEATL-----TMDQVSSILALAKVPPR 67
 QY 71 ERICVFSTSPAKDSIFEDFDLILSVFSDTATPDIKSHYARIRDEDDGTLNEDLSR 130

Db 68 DRICRVFSDH---NVFSEEDVLGMASVSEQACSPKIEVAFRIYDFNENGFIDEEDLE 124
 QY 131 LVNLTGEGEPTRLSASE--MKQILDNILESDIDROGTINLSEFOHYISSRPFASSEFK 188
 Db 125 IVLRLL-KSD-----ASEDLMDVMHHVLSSESDIDNDSMLSFSEFHMAKSPFMNSFR 179
 QY 189 I 189
 Db 180 I 180

RESULT 3

Q96Q77 PRELIMINARY; PRT; 187 AA.
 AC 096Q77;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DE 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
 GN KIP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RA Hayashi A., Okaze H., Kozuma S., Saito T.,
 RT KIP3.
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB050868; BAB71789.1; -.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
 SQ SEQUENCE 187 AA; 21801 MW; FB32CBA46DF5ADCF CRC64;

Query Match 36.0%; Score 346; DB 4; Length 187;
 Best Local Similarity 39.9%; Pred. No. 6.7e-23;
 Matches 77; Conservative 42; Mismatches 62; Indels 12; Gaps 4;

QY 1 MGSGSRSLKELAEYODITFLTKQELILAHRRFCFLPQ-----EQRTVSSILRAQVPE 56
 Db 1 MGKQVFTFHEQLEAVQDCTFFTRKEIMRLFYRQDLAPQLVPIDYTTCD--VKPYE 57
 QY 57 QILSLPELANPKRICKRVSTSPAKDSIFEDFDLILSVFSDTATPDIKSHYARIRFD 116
 Db 58 LLSMPLELDNPRORIAQVFS-EDGGMHTLNFIDMFVSMEMAPRDLKAYAFRIYD 116
 QY 117 FDDGTLNEDLSRYNCLTGEDEDTRLSASEKQILDNILESDIDROGTINLSEFOHY 176
 Db 117 FNNDYICANDLQVTKLTRGG-----LSAEVSLVCEKVLDEAGDHDRLSLDFRQM 172
 QY 177 ISRSPDFASSEFKI 189
 Db 173 ILRAPDFLSFTFI 185

RESULT 4
 Q9W205 PRELIMINARY; PRT; 206 AA.
 AC 09W205;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 GN CG9236 protein.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 RP SEQUENCE FROM N.A.

[illegible]

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DE 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calcineurin b subunit (protein phosphatase 2b regulatory subunit)-like
DE protein (Hypothetical 20.0 kDa protein).
GN Ar3g18430.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneo T., Kato T., Asamizu E., Tabata S.;
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA MEDLINE=20277480; PubMed=10819329;
RX Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty pl and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banb J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamuya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koeseema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene At3g18430 (GI:152296640).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Banb J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamuya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP EMBL; AB026558; BAB01109.1; -
RA EMBL; AY063789; AAL36096.1; -
DR EMBL; AY091287; AAM14226.1; -
HSSP; P06705; IAU1.
DR InterPro: IPR0002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 175 AA; 20032 MW; B26D6F2ADA26AFED CQC64;

Query Match 20.2% Score 194; DB 10; Length 175;
Best Local Similarity 27.2%; Pred. No. 1.6e-09;
Matches 50; Conservative 45; Mismatches 65; Indels 24; Gaps 5;

OY 1 MGGSSRLSKELLAYO---DLFTLTOEILAHRRFCELLPQGRVTESSLAQVPE 56
Db 1 MGNISMLTQYDIEVQSHCHDL--FEQCEILSLYQRFQL-----DRNAKGFISAD 50
OY 57 QILSLPELNAKPFKEIKRVESTSPAKDSLSEDFDLISVSDTATPDINKSHVAFRIED 116
Db 51 EFLSVPEPAMNPLSGRLKKV-----DGLNKKDFVAFLSAASAKASLRQKYLFFKYAD 104
OY 117 FDDDCGLTNRDLSTRLVNCLEGGEDTRLSASEKQOLINIEESPIDRNGTINLSEPOHV 176

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Db 105 SCNKGVSFKDIEMVLRDLSSG-----SPMSDEQREQVLSQVLRKESGYTSDSFLLTDFRIKI 160
 QY 177 ISRS 180
 Db 161 FGSS 164

RESULT 9

Q93VF2 PRELIMINARY; PRT; 175 AA.
 AC Q93VF2;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Calcineurin-like protein.
 GN ECCLBL OR ECCLBL.
 OS Eucalyptus camaldulensis (Murray red gum), and
 OS Eucalyptus grandis.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Myrtales; Myrtaceae; Eucalyptus.
 OX NCBI_TaxID=34316, 71139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.camaldulensis, and E.grandis; TISSUE=FLOWER;
 RA Falibairn D.J., Gomez-Gallego S., Sawbridge T., Teasdale R.D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF197334; AL25650.1;
 DR EMBL; AF197330; AL25647.1;
 DR InterPro; IPR02048; EF-hand.
 DR Pfam; PF00036; ehand; 2.
 DR Prodom; PD000012; EF-hand; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 SQ SEQUENCE 175 AA; 1997 MW; C4E773EE42A3EF16 CRC64;

Query Match 20.1%; Score 193; DB 10; Length 175;
 Best Local Similarity 26.4%; Pred. No. 2e-09;

Matches 48; Conservative 45; Mismatches 69; Indels 20; Gaps 4;

QY 1 MGGSGSRSLKELAEYD--LTFITKOEILAHRRFCCELLPQEQRTVESSLRQAVPEQI 58
 Db 1 MGNSSMLTYDIEVDHCCNNLFSQOEIYSLYERFCOL-----DRNKGFLSDEF 52
 QY 59 LSLPELKANPKERICRVSTSPAKDSLSEDFDLISVSDTATPDIKSHYARIDPD 118
 Db 53 LSVPEFMNPUSORLKMV-----DGLNEKDFVAFLSNFSAKSKCKKTELIRKYVDS 106
 QY 119 DDGTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILESDIDRGTINLSEFOHYS 178
 Db 107 CNGKVSNDILIEVLRDLSSG-----PFMSDEQREQVLSQVLRKESGYTSDSFLLDVFVFG 162
 QY 179 RS 180
 Db 163 NS 164

RESULT 10

Q9NFN1 PRELIMINARY; PRT; 169 AA.
 AC Q9NFN1;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Calcineurin B.
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20520966; PubMed=11071287;
 RA Mecozzi B., Rossi A., Lazaretti P., Kady M., Kaiser S., Valle C.,

RA Cioffi D., Klinkert M.O.;
 RT "Molecular cloning of Schistosoma mansoni calcineurin subunits and
 RT Immunolocalization to the excretory system";
 RL Mol. Biochem. Parasitol. 110:333-343(2000).
 DR EMBL; AJ276885; CAB93677.1;
 DR HSSP; P06705; IMCO
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; ehand; 4.
 DR PRINTS; PR00450; RECOVERIN.
 DR Prodom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
 SQ SEQUENCE 169 AA; 1917 MW; 878E01D08BC5DC1D CRC64;

Query Match 19.2%; Score 184.5; DB 5; Length 169;
 Best Local Similarity 30.1%; Pred. No. 1.1e-08;
 Matches 37; Conservative 32; Mismatches 49; Indels 5; Gaps 2;

QY 56 EQLSLPELKANPKERICRVSTSPAKDSLSEDFDLISVSDTATPDIKSHYARIF 115
 Db 40 KEFMSLPEIQNPVLRVLEIFDQ--GNCEVDKFERKINGMSQFSKGEAKLKAFKIX 98
 QY 116 DEDDGTNREDLSRLVNCITGEGEDTRLASSEMQLIDNILESDIDRGTINLSEFOH 175
 Db 99 DMDKGYISNGBLFGVLRKMVG---NNLKDTLOQIYDKTIFPKDEDRISFEFCE 154
 QY 176 VIS 178
 Db 155 VVS 157

RESULT 11

Q20804 PRELIMINARY; PRT; 244 AA.
 AC Q20804;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE F55C10.1 protein.
 GN F55C10.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dobson R.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;

RA none;
 RT "genome sequence of the nematode C.elegans: A platform for
 RT investigating biology";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z74036; CAA98489.2;
 DR HSSP; P06705; LAUI.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; ehand; 4.
 DR PRINTS; PR00450; RECOVERIN.
 DR Prodom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
 SQ SEQUENCE 244 AA; 27901 MW; 6899CB58CB77D08B CRC64;

Query Match 19.1%; Score 183.5; DB 5; Length 244;
 Best Local Similarity 27.8%; Pred. No. 2.1e-08;
 Matches 50; Conservative 38; Mismatches 69; Indels 23; Gaps 6;

QY 3 GSGSRSLKELAEYD--LTFITKOEILAHRRFCCELLPQEQRTVESSLRQAVPEQIIS 60
 Db 1 MGNSSMLTYDIEVDHCCNNLFSQOEIYSLYERFCOL-----DRNKGFLSDEF 52


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DB      2 GNENSLPMEIACSNFD-----PDEIKRLGKRF-----RKLDLNSGSLSVDEFMLLP 47
QY      63 ELKANPFEKRICRYSTSPAKDSLSEDFDLISVFSPTAPDLSHYAFRIFFDDGT 122
DB      48 ELQONPPLVQRYVIDFTD-GNGEVDKFEKIEGVSOFSVKGDKSLRFAFKIYDMDDKG 106
QY      123 LNRDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFQHYI 177
DB      107 ISNGELFVGLKMWG-----NNLKDTQLQOIYDKTIHADADGDKISFEFCAYV 157

RESULT 14
Q95P81  PRELIMINARY;      PRT;      170 AA.
ID      095P81
AC      095P81
DT      01-DEC-2001 (TREMBLrel. 19, 1streated)
DT      01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE      Calcineurin B.
GN      CNB.
OS      Bombyx mori (Silk moth).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC      Bombycoidea; Bombycidae; Bombyx.
OX      NCBI_Taxid=7091;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=SHUKO X RYUAKU; TISSUE=PEROMONE GLAND;
RA      Yoshiga T., Matsumoto S.;
RT      "cDNA cloning of heterosubunits of calcineurin from pheromone gland of
RT      Bombyx mori."
RL      Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF287251; AAK83039.1; -
DR      InterPro: IPR002048; EF-hand.
DR      Pfam: PF00036; ehand; 4.
DR      ProDom: PD000012; EF-hand; 2.
DR      PROSITE: PS00018; EF-HAND; UNKNOWN_4.
SQ      SEQUENCE 170 AA; 19357 MW; 5EC15B820097130 CRC64;

Query Match      18.8%; Score 180.5; DB 5; Length 170;
Best Local Similarity 24.7%; Pred. No. 2.4e-08;
Matches 44; Conservative 44; Mismatches 71; Indels 19; Gaps 4;

QY      3 GSGRLSKELLAEQDITFLKQETLAHRRFCCLLPQEQRTVSSLRQVPEEQILSLP 62
DB      2 GNENSLPMEIACSNFD-----ADEIRLGRKF-----RKLDLNSGSLSVDEFMLLP 47
QY      63 ELKANPFEKRICRYSTSPAKDSLSEDFDLISVFSPTAPDLSHYAFRIFFDDGT 122
DB      48 ELQONPPLVQRYVIDFTD-ADGNGEVDKFEKIEGVSOFSVKGDKSLRFAFKIYDMDDKG 106
QY      123 LNRDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFQHYISRS 180
DB      107 ISNGELFVGLKMWG-----NNLKDTQLQOIYDKTIHADADGDKISFEFCAYV 160

RESULT 15
Q99LQ9  PRELIMINARY;      PRT;      115 AA.
ID      099LQ9
AC      099LQ9
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE      Hypothetical 13.1 kDa protein.
GN      PPP3R1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
OX      NCBI_Taxid=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      Strausberg R.;
RA      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

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DR      EMBL; BC002267; AA02267.1; -.
DR      HSSP; P06705; IAO1.
DR      MGD; MGI:107172; Ppp3r1.
DR      InterPro: IPR002048; EF-hand.
DR      InterPro: IPR001125; Recoverin.
DR      Pfam; PF00036; ehand; 3.
DR      PRINTS; PR00450; RECOVERIN.
DR      ProDom; PD000012; EF-hand; 2.
DR      SMART; SM00054; EFh; 3.
DR      PROSITE; PS00018; EF-HAND; UNKNOWN_3.
KW      Hypothetical protein.
SQ      SEQUENCE 115 AA; 13134 MW; B3E1734C07A65471 CRC64;

Query Match      18.5%; Score 177.5; DB 11; Length 115;
Best Local Similarity 31.3%; Pred. No. 2.7e-08;
Matches 36; Conservative 30; Mismatches 44; Indels 5; Gaps 2;

QY      59 LSLPLKANPFEKRICRYSTSPAKDSLSEDFDLISVFSPTAPDLSHYAFRIFFD 118
DB      1 MSLPQLQONPPLVQRYVIDFTD-GNGEVDKFEKIEGVSOFSVKGDKSLRFAFKIYDM 59
QY      119 DDGTLNRDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEF 173
DB      60 KDGTISNGELFVGLKMWG-----NNLKDTQLQOIYDKTIHADADGDKISFEFCAYV 110

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Search completed: November 21, 2002, 17:58:51
 Job time : 33 secs

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OM protein - protein search, using sw model

Run on: November 21, 2002, 17:57:51 : Search time 15 Seconds

(without alignments)
374.652 Million cell updates/sec

Title: US-09-878-454A-2

Perfect score: 962
Sequence: 1 MGSGSRSLSKLLAEYODLT.....EFQHVIRSPDFASSFKIVL 191

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	958	99.6	191	4	US-08-720-625-2
2	952	99.0	191	3	US-08-764-563-1
3	216.5	22.5	177	3	US-08-764-563-3
4	204.5	21.3	174	1	US-08-328-322-17
5	193.5	20.1	157	1	US-08-328-322-15
6	186.5	19.4	159	4	US-08-720-625-4
7	186.5	19.4	170	3	US-08-764-563-5
8	176	18.3	186	4	US-08-655-352-8
9	176	18.3	186	4	US-09-258-016-8
10	176	18.3	186	4	US-09-257-825B-8
11	172.5	17.9	179	3	US-08-764-563-4
12	153.5	16.0	196	3	US-09-048-889-1
13	150	15.6	193	3	US-08-655-352-3
14	150	15.6	193	4	US-09-258-016-3
15	150	15.6	193	4	US-09-257-825B-3
16	146	15.2	220	4	US-09-399-913-26
17	146	15.2	220	4	US-09-298-731-26
18	142	14.8	211	3	US-08-655-352-7
19	142	14.8	191	4	US-09-258-016-7
20	142	14.8	191	4	US-09-257-825B-7
21	141	14.7	220	4	US-09-399-913-24
22	141	14.7	220	4	US-09-298-731-24
23	141	14.7	252	4	US-09-399-913-20
24	141	14.7	252	4	US-09-298-731-20
25	141	14.7	270	4	US-09-399-913-14
26	141	14.7	270	4	US-09-298-731-14
27	139	14.4	193	3	US-08-655-352-2

28	139	14.4	193	4	US-09-258-016-2	Sequence 2, Appl1
29	138	14.3	193	4	US-09-257-825B-2	Sequence 2, Appl1
30	138	14.3	216	4	US-09-399-913-6	Sequence 6, Appl1
31	138	14.3	216	4	US-09-298-731-6	Sequence 6, Appl1
32	138	14.3	227	4	US-09-399-913-8	Sequence 8, Appl1
33	138	14.3	227	4	US-09-399-913-10	Sequence 10, Appl1
34	138	14.3	227	4	US-09-298-731-8	Sequence 8, Appl1
35	138	14.3	227	4	US-09-399-913-10	Sequence 10, Appl1
36	138	14.3	245	4	US-09-399-913-4	Sequence 4, Appl1
37	138	14.3	245	4	US-09-298-731-4	Sequence 4, Appl1
38	138	14.3	270	4	US-09-399-913-18	Sequence 18, Appl1
39	138	14.3	270	4	US-09-298-731-18	Sequence 18, Appl1
40	137	14.2	216	4	US-09-399-913-2	Sequence 2, Appl1
41	137	14.2	216	4	US-09-298-731-2	Sequence 2, Appl1
42	136	14.1	225	4	US-09-399-913-30	Sequence 30, Appl1
43	136	14.1	225	4	US-09-298-731-30	Sequence 30, Appl1
44	136	14.1	252	4	US-09-399-913-22	Sequence 22, Appl1
45	136	14.1	252	4	US-09-399-913-22	Sequence 28, Appl1

ALIGNMENTS

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RESULT 1
US-08-720-625-2
; Sequence 2, Application US/08720625
; Patent No. 6242587
; GENERAL INFORMATION:
; APPLICANT: Naik, Ulhas P.
; TITLE OF INVENTION: CALCIUM-INTERGRIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: NC 28234
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,625
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-138
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3175
; TELEFAX: 919-420-2200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-720-625-2

Query Match          99.6%  Score 958;  DB 4;  Length 191;
Best Local Similarity 99.5%  Pred. No. 1.6e-97;
Matches 190;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

QY  1  MGSGSRSLSKLLAEYODLTFLKOEILLARRFELLPOEORTVESSLRAOVPEQILS 60
    |||
Db  1  MGSGSRSLSKLLAEYODLTFLKOEILLARRFELLPOEORTVESSLRAOVPEQILS 60
QY  61 LPELKNPFKRIKRVSTSPAKOSLSFEDLLSVSDTATPDIKSHYAFRIEDFDD 120
    |||

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Db 61 LPELKNPFRKRICRVSTSPADSLSFEDFLDLVSFSDTATPDIKSHAFRIPEDDDD 120
QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHAYSRS 180
Db 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHAYSRS 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 2

US-08-764-563-1
; Sequence 1, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
US-08-764-563-1

Query Match 99.0%; Score 952; DB 3; Length 191;
Best Local Similarity 99.0%; Pred. No. 7.2e-97;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELAEYODTLFLKQELLAHRRFCCLLPQEQRTVSSSLRAQVPEOILS 60
Db 1 MGGSGSRLSKELAEYODTLFLKQELLAHRRFCCLLPQEQRTVSSSLRAQVPEOILS 60
QY 61 LPELKNPFRKRICRVSTSPADSLSFEDFLDLVSFSDTATPDIKSHAFRIPEDDDD 120
Db 61 LPELKNPFRKRICRVSTSPADSLSFEDFLDLVSFSDTATPDIKSHAFRIPEDDDD 120
QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHAYSRS 180
Db 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHAYSRS 180

QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 3

US-08-764-563-3
; Sequence 3, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 458230
US-08-764-563-3

Query Match 22.5%; Score 216.5; DB 3; Length 177;
Best Local Similarity 29.2%; Pred. No. 4.1e-16;
Matches 52; Conservative 40; Mismatches 73; Indels 13; Gaps 3;

QY 1 MGGSGSRLSKELAEYODTLFLKQELLAHRRFCCLLPQEQRTVSSSLRAQVPEOILS 60
Db 1 MGTNTSLRPEEVEEMQKGNFTQKEIKLKKRKDKDNGNGTISK-----DEFLM 52
QY 61 LPELKNPFRKRICRVSTSPADSLSFEDFLDLVSFSDTATPDIKSHAFRIPEDDDD 120
Db 53 IPELANPFLKRVISIFDEN-GGGSVNFKEFFIALSVFNAGDKQKLEFRFKYDIDGD 111
QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHAYSRS 178
Db 112 GYISNGELFVLKMMVG-----NNLSDVQIQIYDKTILAEDEGDKKISFEFFAKTIS 165
RESULT 4
US-08-328-322-17
; Sequence 17, Application US/08328322

Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-17

Query Match 21.3%; Score 204.5; DB 1; Length 174;
Best Local Similarity 27.1%; Pred. No. 8.2e-15;
Matches 48; Conservative 44; Mismatches 68; Indels 17; Gaps 4;
QY 1 MGGGSRSLKELAEYDPLTRKOEILAHRCCELLPOQRVYESSLRQVFEQILS 60
DB 1 MGAAPSRIYVGLD-----TFNDELELRKRMKIDRSSGSSIDKN-----EFMS 48
QY 61 LPELKANPFRICRVSTSPAKDSLSEFEDLLSVSPDTPDKSHVAFRIFEDDD 120
DB 49 IPGVSSNPGLRIMEVFDADNSGD-VDFQEFITGLSIFSGSKDEKLRFKIIDDKD 107
QY 121 GLURRLSLVNLGEGEDTRLSASEMKQILNIEESDIDRDGTINLSEFOHVI 177
DB 108 GFISNGELFYVLIKWG-----SNLDDQLQOIVDRITVENDSDGRLSFEFKNAI 160

RESULT 5
US-08-328-322-15
Sequence 15, Application US/08328322
Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-15

Query Match 20.1%; Score 193.5; DB 1; Length 157;
Best Local Similarity 27.3%; Pred. No. 1.1e-13;
Matches 42; Conservative 40; Mismatches 59; Indels 13; Gaps 3;
QY 24 KOEILAHRCCELLPOQRVYESSLRQVFEQILSPELKANPFRICRVSTSPAK 83
DB 3 RDEIFRLKRMKIDRSSGSSIDKN-----EFMSIPGVSSNPGLRIMEVFDADNSG 54
QY 84 DLSFEEDLLSVSPDTPDKSHVAFRIFEDDDTINLEDLSRLVNCUTGGEEDPR 143
DB 55 D-VDFQEFITGLSIFSGSKDEKLRFKIIDDKDGFISNGELFYVLIKWG-----SN 109
QY 144 LSASEMKQILNIEESDIDRDGTINLSEFOHVI 177
DB 110 LDDQLQOIVDRITVENDSDGRLSFEFKNAI 143

RESULT 6
US-08-720-625-4
Sequence 4, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Nalk, Ulhas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sidley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-861-3175
INFORMATION FOR SEQ ID NO: 4:

Query Match 19.48; Score 186.5; DB 3; Length 170;

Dy 1 MGGSGSRSKELLLEYQDTFTLTKEIILAHRRCELLPOEORTVESSLRAQVPEEQILS 60
|||:::|||||:
Db 1 MGKSSSKAQDIDRLTTDTFTEKEIRQMHWKGFLKDCPNLLTDEGPIKITKOF----- 55

QY 61 LPELKANPKEKRICVSTSPAKDSLSEDFDLDSVSDTAPDPKSHYAFRIFEDDD 120
 DB 56 FPGDPSKFAISLVFVFDEN-NDGSIIEFEERFALSVTSKGL--DEKLOMARLVYDND 112
 QY 121 GTLNREDLSRLVNC-----TGEGDTRLASASEMKOLINILEESIDIDRGITINLSE 172
 DB 113 GYITREEMYNIVDAIYQWGOQPOSEDENT-----PQKRVKIDFQDMKNHDKLTLEE 166
 QY 173 FOHVISRSPDPASSFKI 189
 DB 167 FREGSKADPRIVQALSL 183

RESULT 9

US-09-258-016-8
 ; Sequence 8, Application US/09258016
 ; Patent No. 6362395
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachettira W. Poovalah, Zhinua Liu,
 ; APPLICANT: Shameekumar Patil, Daisuke Takezawa
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; PRODUCTION OF MALE-STERILE PLANTS
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kiarquist Sparkman Campbell Leigh &
 ; ADDRESSEE: Whinston, LLP
 ; STREET: One World Trade Center
 ; STREET: 121 S.W. Salmon Street
 ; STREET: Suite 1600
 ; CITY: Portland
 ; STATE: Oregon
 ; COUNTRY: United States of America
 ; ZIP: 97204
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Disk, 3-1/2 inch
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/258,016
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stephens Jr., Donald L.
 ; REGISTRATION NUMBER: 34,022
 ; REFERENCE/DOCKET NUMBER: 4630-51994
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (503) 226-7391
 ; TELEFAX: (503) 228-9446
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 186 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; DESCRIPTION: Region of Drosophila frequenin
 ; (Gen2:Drofreg) with homology to 111y
 ; DESCRIPTION: CCAMK
 ; US-09-258-016-8

Query Match 18.3%; Score 176; DB 4; Length 186;
 Best Local Similarity 25.4%; Pred. No. 1.2e-11;
 Matches 50; Conservative 40; Mismatches 85; Indels 22; Gaps 5;

QY 1 MGSGSRSLSEKLLAEYODLTFTKOEILAHARFCELLPOEQRVTESSLRQAQVPEQILS 60
 DB 1 MGKSSKRLKODTIDRLTDTYFTEKEIKRQWKGFLKDCPNGLTDEGFIKITKQF----- 55
 QY 61 LPELKANPKEKRICVSTSPAKDSLSEDFDLDSVSDTAPDPKSHYAFRIFEDDD 120
 DB 56 FPGDPSKFAISLVFVFDEN-NDGSIIEFEERFALSVTSKGL--DEKLOMARLVYDND 112

QY 121 GTLNREDLSRLVNC-----TGEGDTRLASASEMKOLINILEESIDIDRGITINLSE 172
 DB 113 GYITREEMYNIVDAIYQWGOQPOSEDENT-----PQKRVKIDFQDMKNHDKLTLEE 166
 QY 173 FOHVISRSPDPASSFKI 189
 DB 167 FREGSKADPRIVQALSL 183

RESULT 10

US-09-257-825B-8
 ; Sequence 8, Application US/09257825B
 ; Patent No. 6403352
 ; GENERAL INFORMATION:
 ; APPLICANT: Poovalah, Bachettira W.
 ; APPLICANT: Patil, Shameekumar
 ; APPLICANT: Takezawa, Daisuke
 ; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plan
 ; FILE REFERENCE: 4630-51993
 ; CURRENT APPLICATION NUMBER: US/09/257,825B
 ; CURRENT FILING DATE: 1999-02-25
 ; PRIOR APPLICATION NUMBER: US 08/655,352
 ; PRIOR FILING DATE: 1996-05-23
 ; PRIOR APPLICATION NUMBER: US 60/014,743
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 186
 ; TYPE: PRT
 ; ORGANISM: Drosophila
 ; US-09-257-825B-8

Query Match 18.3%; Score 176; DB 4; Length 186;
 Best Local Similarity 25.4%; Pred. No. 1.2e-11;
 Matches 50; Conservative 40; Mismatches 85; Indels 22; Gaps 5;

QY 1 MGSGSRSLSEKLLAEYODLTFTKOEILAHARFCELLPOEQRVTESSLRQAQVPEQILS 60
 DB 1 MGKSSKRLKODTIDRLTDTYFTEKEIKRQWKGFLKDCPNGLTDEGFIKITKQF----- 55
 QY 61 LPELKANPKEKRICVSTSPAKDSLSEDFDLDSVSDTAPDPKSHYAFRIFEDDD 120
 DB 56 FPGDPSKFAISLVFVFDEN-NDGSIIEFEERFALSVTSKGL--DEKLOMARLVYDND 112
 QY 121 GTLNREDLSRLVNC-----TGEGDTRLASASEMKOLINILEESIDIDRGITINLSE 172
 DB 113 GYITREEMYNIVDAIYQWGOQPOSEDENT-----PQKRVKIDFQDMKNHDKLTLEE 166
 QY 173 FOHVISRSPDPASSFKI 189
 DB 167 FREGSKADPRIVQALSL 183

RESULT 11

US-08-764-563-4
 ; Sequence 4, Application US/08764563
 ; Patent No. 6093565
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible

```

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,563
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0178 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 109612
US-08-764-563-4

```

```

Query Match      17.9%; Score 172.5; DB 3; Length 179;
Best Local Similarity 27.8%; Pred. No. 2.8e-11;
Matches 42; Conservative 30; Mismatches 66; Indels 13; Gaps 3;

```

```

QY 35 CELLP0EQ-----RTVESLSRAQVPEPOLSLPELKNPKERICRFVSPAKDSL 86
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
DB 12 CNFDEBEIRLKRKRLDLDKSGSLTEFRRLPELQNPVGRVIDFTD-NGEYV 70
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
QY 87 SFEDFLDLVSFSDTATPPDIKSHYARIPDDDTGLNREDSRLVNCLTGEGEDPRLSA 146
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
DB 71 DPEFTVGTQSOFVKGDEQKLRFAFRIVDMNDGFIISNELFOVLMKMG-----NNLKD 126
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
QY 147 SEKKQIDNLTESDIDRGITINLSFQAVI 177
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
DB 127 WQLQQLVDSILVLDKDGGRISFEFSDVY 157
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |

```

```

RESULT 12
US-09-048-889-1
Sequence 1, Application US/09048889
Patent No. 6117989
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lal, Preeti
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,889
FILING DATE: Herewith

```

```

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0493 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNCT09
CLONE: 1846517
US-09-048-889-1

```

```

Query Match      16.0%; Score 153.5; DB 3; Length 196;
Best Local Similarity 23.3%; Pred. No. 3.9e-09;
Matches 44; Conservative 39; Mismatches 73; Indels 33; Gaps 6;

```

```

QY 5 GSRLSKELAEYODL---TEFLAKQELILAHRRPCELLPOEORTVESLSRAQVPEOILS 60
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
DB 2 GSRTSHAAVIPDGSIRRTGFGSASLRLHNR-----RLDNKKKCYLSRMLDQ 53
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
QY 61 LPELKNPKERICRVSTSPAKDSLSEFEDFLDLVSF-----SDTATPDIK----- 108
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
DB 54 IGALAVNPDLDRITIESEFPG-GSORVDFPGFVRVLAHFRPYEDDETFTODPKKPEPLNSR 112
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
QY 109 ----HYAFRFDPPDDDTLNRREDSRLVNCLTGEGEDPRLSASMKQIDNLTESDIDR 164
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
DB 113 RNLHLVAFOLXIDDRDKIRHEMLVRLMVG-----VQYTEOENIADRTVOEADBOG 168
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
QY 165 DGTINLSEF 173
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |
DB 169 DGAVSFEVF 177
| 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: | 11: |

```

```

RESULT 13
US-08-655-352-3
Sequence 3, Application US/08655352
Patent No. 6077991
GENERAL INFORMATION:
APPLICANT: Bachettira W. Poovalah, Zhilua Liu,
APPLICANT: Shameekumar Patil, Dalsuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:
CLASSIFICATION: 800

```



```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of rat neural visinin-like protein
DESCRIPTION: (Gen2:Ratnvp3) with homology to 11ly
DESCRIPTION: CCAMK
US-08-655-352-3

Query Match      15.6%; Score 150; DB 3; Length 193;
Best Local Similarity 24.5%; Pred. No. 9.3e-09;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELAEYODLFTLKQELLAHRRFCCLLPQEQRTVSSLRQVFEQILS 60
  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 1 MGKQNSKRLRPVLDLREHTEFTDHELOEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELANPFRICRVSTSPAKDSLSEFEDLDLSVFSDDTATPDIKSHYAFRIPDF 118
  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 54 NEFPYGDASKFAEHVFTFDIN-SDGTIDREFITALSVTS-RGKLEQKIKMAFSWYDLD 111

QY 119 DDGLTNEDLSRLVNCLTGEGEDTRLASASEK-----QLDNLIESDDIDRGTIN 169
  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 112 GNGTISRSEMLEIVQAI-----YKMWSSVKMPEDESTPEKRDKIFRQMDINNDGKLS 165

QY 170 LSEF-----QHVISRSPDFASSF 187
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DB 166 LEFPIKAKSDPSIVRLQCDPSSASQF 193

RESULT 14
US-09-258-016-3
; Sequence 3, Application US/09258016
; Patent No. 6362395
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovalah, Zhuhua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klargust Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible-
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,016
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephens Jr., Donald L.

```

```

REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630-51994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Region of rat neural visinin-like protein
DESCRIPTION: (Gen2:Ratnvp3) with homology to 11ly
DESCRIPTION: CCAMK
US-09-258-016-3

Query Match      15.6%; Score 150; DB 4; Length 193;
Best Local Similarity 24.5%; Pred. No. 9.3e-09;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELAEYODLFTLKQELLAHRRFCCLLPQEQRTVSSLRQVFEQILS 60
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DB 1 MGKQNSKRLRPVLDLREHTEFTDHELOEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELANPFRICRVSTSPAKDSLSEFEDLDLSVFSDDTATPDIKSHYAFRIPDF 118
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DB 54 NEFPYGDASKFAEHVFTFDIN-SDGTIDREFITALSVTS-RGKLEQKIKMAFSWYDLD 111

QY 119 DDGLTNEDLSRLVNCLTGEGEDTRLASASEK-----QLDNLIESDDIDRGTIN 169
  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 112 GNGTISRSEMLEIVQAI-----YKMWSSVKMPEDESTPEKRDKIFRQMDINNDGKLS 165

QY 170 LSEF-----QHVISRSPDFASSF 187
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DB 166 LEFPIKAKSDPSIVRLQCDPSSASQF 193

RESULT 15
US-09-257-825B-3
; Sequence 3, Application US/09257825B
; Patent No. 6403352
; GENERAL INFORMATION:
; APPLICANT: Poovalah, Bachettira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plan
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257,825B
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655,352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014,743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Rat
; US-09-257-825B-3

Query Match      15.6%; Score 150; DB 4; Length 193;
Best Local Similarity 24.5%; Pred. No. 9.3e-09;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELAEYODLFTLKQELLAHRRFCCLLPQEQRTVSSLRQVFEQILS 60
  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
DB 1 MGKQNSKRLRPVLDLREHTEFTDHELOEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELANPFRICRVSTSPAKDSLSEFEDLDLSVFSDDTATPDIKSHYAFRIPDF 118
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DB 54 NEFPYGDASKFAEHVFTFDIN-SDGTIDREFITALSVTS-RGKLEQKIKMAFSWYDLD 111

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Thu Nov 21 18:12:51 2002

us-09-878-454a-2.rai

Page 8

[illegible]

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Search completed: November 21, 2002, 17:59:54
Job time : 16 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2002, 17:58:20 ; Search time 11 Seconds
(without alignments)
271.941 Million cell updates/sec

Title: US-09-878-454A-2
Perfect score: 962
Sequence: 1 MGSGSRLSKELLAEYQDIT.....EFQHVSRPDSFKIYV 191

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications-AA:*
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7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	962	100.0	191	10	US-09-878-454A-2
2	950	98.8	191	12	US-10-109-885-2
3	345	35.9	187	10	US-09-802-116-2
4	186.5	19.4	170	12	US-10-109-885-3
5	179.5	18.7	195	10	US-09-999-602-3
6	174.5	18.1	195	10	US-09-999-602-4
7	146	15.2	220	10	US-09-350-874-10
8	141	14.7	220	10	US-09-350-874-16
9	141	14.7	220	10	US-09-350-874-24
10	141	14.7	220	10	US-09-350-874-20
11	138	14.3	216	10	US-09-350-874-14
12	138	14.3	216	10	US-09-350-874-6
13	138	14.3	227	10	US-09-350-874-8
14	138	14.3	227	10	US-09-350-874-10
15	138	14.3	245	10	US-09-350-874-4
16	137	14.2	270	10	US-09-350-874-18
17	136.5	14.2	216	10	US-09-350-874-2
18	136	14.1	225	10	US-09-999-602-1
19	136	14.1	252	10	US-09-350-874-30
20	136	14.1	252	10	US-09-350-874-22

20	136	14.1	252	10	US-09-350-874-28	Sequence 28, Appl
21	136	14.1	252	10	US-09-350-874-42	Sequence 42, Appl
22	136	14.1	257	10	US-09-350-874-16	Sequence 16, Appl
23	126	13.1	229	10	US-09-350-874-70	Sequence 70, Appl
24	126	13.1	233	10	US-09-350-874-49	Sequence 49, Appl
25	126	13.1	250	10	US-09-350-874-72	Sequence 72, Appl
26	113.5	11.8	1210	10	US-09-922-217-692	Sequence 692, App
27	113.5	11.8	1210	10	US-09-833-263-692	Sequence 692, App
28	113.5	11.8	1548	10	US-09-922-217-1095	Sequence 1095, App
29	112.5	11.7	172	12	US-10-109-885-4	Sequence 4, Appl1
30	112	11.6	256	10	US-09-350-874-32	Sequence 32, Appl
31	111.5	11.6	142	10	US-09-910-071-4	Sequence 4, Appl1
32	110	11.4	203	10	US-09-350-874-12	Sequence 12, Appl
33	110	11.4	642	9	US-09-554-000-2	Sequence 2, Appl1
34	110	11.4	652	9	US-09-554-000-4	Sequence 4, Appl1
35	109	11.3	256	10	US-09-350-874-36	Sequence 36, Appl
36	108	11.2	642	9	US-09-554-000-6	Sequence 6, Appl1
37	108	11.2	656	9	US-09-554-000-8	Sequence 8, Appl1
38	107.5	11.2	159	10	US-09-910-071-5	Sequence 5, Appl1
39	107.5	11.2	201	10	US-09-925-297-714	Sequence 714, App
40	102.5	10.7	139	10	US-09-864-761-34808	Sequence 34808, A
41	95.5	9.9	90	10	US-09-826-589-3	Sequence 3, Appl1
42	95.5	9.9	90	10	US-09-826-589-4	Sequence 4, Appl1
43	95.5	9.9	90	10	US-09-872-1858-11	Sequence 11, Appl
44	95.5	9.9	90	10	US-09-872-1858-12	Sequence 12, Appl
45	95	9.9	1604	10	US-09-888-615-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-09-878-454A-2
Sequence 2, Application US/09878454A
Patent No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Montelito, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentin
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-2

Query Match 100.0%; Score 962; DB 10; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MGSGSRLSKELLAEYQDITFLTKOETLAHRRFCETLPOEORVSSLSRAQVPEFGLS	60
QY	61	LEELKANPKERICRVSTSPANDSLFEDFDLVSFSDTAPDLSHYAFIFPDD	120
DB	61	LEELKANPKERICRVSTSPANDSLFEDFDLVSFSDTAPDLSHYAFIFPDD	120
QY	121	GLTNREDSRLVNCLEGEEDRTLSSEKQIDNLEESDIDRGTINSEFQVHSRS	180
DB	121	GLTNREDSRLVNCLEGEEDRTLSSEKQIDNLEESDIDRGTINSEFQVHSRS	180
QY	181	PDFASSFKIVL 191	
DB	181	PDFASSFKIVL 191	

RESULT 2

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US-10-109-885-2
: Sequence 2, Application US/10109885
: Patent No. US20020119129A1
: GENERAL INFORMATION:
:   APPLICANT: REVEL, Michel
:   APPLICANT: CHEBATH, Judith
:   APPLICANT: ABRAMOVITCH, Carolina
:   TITLE OF INVENTION: NOVEL IYR RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METHOD OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
:   FILE REFERENCE: REVEL-14A
:   CURRENT APPLICATION NUMBER: US/10/109,885
:   CURRENT FILING DATE: 2002-04-01
:   PRIOR APPLICATION NUMBER: US/09/341,640
:   PRIOR FILING DATE: 1999-10-18
:   PRIOR APPLICATION NUMBER: PCT/US98/00671
:   PRIOR FILING DATE: 1998-01-15
:   PRIOR APPLICATION NUMBER: US 60/035,636
:   PRIOR FILING DATE: 1997-01-15
:   NUMBER OF SEQ ID NOS: 13
:   SOFTWARE: PatentIn version 3.1
:   SEQ ID NO 2
:   LENGTH: 191
:   TYPE: PRY
:   ORGANISM: Homo sapiens
US-10-109-885-2

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Query Match	98.8%;	Score 950;	DB 12;	Length 191;
Best Local Similarity	99.0%;	Pred. No. 3.7e-88;		
Matches 189; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0

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QY	61	LPELKANPF	KRICRVST	SPAKDSLSF	EDFLDL	SVSTAPAT	PDIKSHAF	RI
Db	61	LPELKANPF	KRICRVST	SPAKDSLSF	EDFLDL	SVSTAPAT	PDIKSHAF	RI
QY	121	GTLNREDL	SRVYNC	LTEGEGED	TRLSASE	KQOLIDY	GT	EE
Db	121	GTLNREDL	SRVYNC	LTEGEGED	TRLSASE	KQOLIDY	GT	EE
QY	181	PDFASSFK	IVL	191				
Db	181	PDFASSFK	IVL	191				

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RESULT 3
US-09-802-116-2
; Sequence 2, Application US/09802116
; Patient NO. US20020082406A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020082406A1 Human Kinase Interacting Protein and Polynucleotide
; TITLE OF INVENTION: the Same
; FILE REFERENCE: LEX-0146-USA
; CURRENT APPLICATION NUMBER: US/09/802.116
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/187,719
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-802-116-2

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Query Match	35.9%	Score 345;	DB 10;	Length 187;
Best Local Similarity	40.4%	Pred. No. 1.6e-27;		
Matches 78; Conservative	42;	Mismatches 61;	Indels 12;	Gaps 5;

[illegible]

RESULT 4
 US-10-109-885-3
 : Sequence 3, Application US/10109885
 : Patent No. US20020119129A1
 : GENERAL INFORMATION:
 :
 : APPLICANT: REVEL, Michel
 : APPLICANT: CHEBATH, Judith
 : APPLICANT: ABRAMOVITCH, Carolina
 : TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
 : TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
 : FILE REFERENCE: REVEL-11A
 : CURRENT APPLICATION NUMBER: US/10/109,885

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PRIORITY APPLICATION NUMBER: US/09/341,640
PRIORITY FILING DATE: 1999-10-18
PRIORITY APPLICATION NUMBER: PCT/US98/00671
PRIORITY FILING DATE: 1998-01-15
PRIORITY APPLICATION NUMBER: US 60/035,636
PRIORITY FILING DATE: 1997-01-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 170
TYPE: PRY
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-109-885-3

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	Query Match	19.4%	Score 186.5	DB 12	Length 170:
	Best Local Similarity	31.1%	Pred. No. 1.1e-11;		
	Matches 30; Conservative 32; Mismatches 47; Indels 5; Gaps				
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	: : : : : : : : : : : : : : : :				
Dd	41 EEFSLDELQONPLVNGAVIDIFDID -ONGEVDFREFLEGVSQFSVKDKRQKLRFARIRY 99				
QY	116 DFDDGLTNREDLSRLYNCLTGBCEDTRLASAEKKQLIDNILEESDIDRDGTLNSEFH 175				
	: : : : : : : : : : : : : : : : : : : : :				
Dd	100 DMDKDGYISNCELTQVLKMMVG---NNLKDTOLQOIYVDKTIINADKDGGRISFEFCA 155				
QY	176 VI 177				
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Dd	156 VV 157				

RESULT 5
 US-09-999-602-3
 ; Sequence 3, Application US/09999602
 ; Patent No. US20020091084A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti G.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
 ; FILE REFERENCE: PF-0466-2 CON

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;; CURRENT APPLICATION NUMBER: US/09/999,602
;; CURRENT FILING DATE: 2001-10-25
;; PRIOR APPLICATION NUMBER: 09/010,378
;; PRIOR FILING DATE: 1998-01-21
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PERL Program
;; SEQ ID NO: 3
;; LENGTH: 195
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: Incyte ID No. US20020091084A1 g1226242
US-09-999-602-3
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Best Local Similarity 26.7%; Score 179.5; DB 10; Length 195;
Matches 52; Conservative 36; Mismatches 78; Indels 29; Gaps 6;
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QY 60 SLPELKANPEKERICRVSTSPANDSLSEDFLDSVF-----SDTATPD----- 105
D 53 RIPELAIMPIDRILNAF-FSEGEDQVNRGFMRTLAHFRLEDNEKSKDVNGPEPLNSR 111
QY 106 -IKSHYARIEDPDODGTLNREDLSRLVNCITGEGEDTRLASSEMKOLIDNILESDIR 164
D 112 SNKLFHFRLYDLDKDDKIDSHDQLVLRMVG-----VNISDEQLGSIDARTIQEADQDG 167
QY 165 DGTINLSEFOHVISR 179
D 168 DSAISFTFEPVKYLEK 182
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RESULT 6
US-09-999-602-4
; Sequence 4, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
; CURRENT APPLICATION NUMBER: US/09/999,602
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/010,378
; PRIOR FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO: 4
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020091084A1 g1706967
US-09-999-602-4
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Query Match
Best Local Similarity 18.1%; Score 174.5; DB 10; Length 195;
Matches 51; Conservative 36; Mismatches 79; Indels 29; Gaps 6;
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D 1 MGSRASTLLRDELEIEIKKGFHSQITRLYSRTSLDKENGTLR-----EDFQ 52
QY 60 SLPELKANPEKERICRVSTSPANDSLSEDFLDSVF-----SDTATPD----- 105
D 53 RIPELAIMPIDRILNAF-FSEGEDQVNRGFMRTLAHFRLEDNEKSKDVNGPEPLNSR 111
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QY 106 -IKSHYARIEDPDODGTLNREDLSRLVNCITGEGEDTRLASSEMKOLIDNILESDIR 164
D 112 SNKLFHFRLYDLDKDDKIDSHDQLVLRMVG-----VNISDEQLGSIDARTIQEADQDG 167
QY 165 DGTINLSEFOHVISR 179
D 168 DSAISFTFEPVKYLEK 182
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RESULT 7
US-09-350-874-26
; Sequence 26, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNT-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 26
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Simian sp.
US-09-350-874-26
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Query Match
Best Local Similarity 15.2%; Score 146; DB 10; Length 220;
Matches 44; Conservative 45; Mismatches 81; Indels 14; Gaps 5;
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QY 11 ELLAYODLFTLKQELLARRECELLPOEQRTVESSLRAQVFEQILS--LPELKANP 68
D 41 EGLELOEQRTKTRKELQVLRGFKNECP-----SGIVNEENKQIYSEFFQDDEST 93
QY 69 EKERICRVSTSPANDSLSEDFLDSVFSDTATPDIKSHYARIEFPDDGLNRE-- 126
D 94 YATFLNAPDIN-HDGSVFEDFVAGLSVIL-RGTVDRLWAFNLYDLNRDGCITKDEM 151
QY 127 -DISRLVNCITGEGEDTRLASSEMKOLIDNILESDIDRGTINLSEFOHVISRSPDFAS 185
D 152 LDIKRSIYDMGKYTYPALREAPREHVENFQAMDRNKDVVILEEIESQDENIMR 211
QY 186 SFKI 189
D 212 SMOL 215
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RESULT 8
US-09-350-874-24
; Sequence 24, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNT-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
```

```

; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-874-24

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Query Match      14.7%  Score 141;  DB 10;  Length 220;
Best Local Similarity 23.4%  Pred. No. 5.6e-07;
Matches 43;  Conservative 46;  Mismatches 81;  Indels 14;  Gaps 5;

```

```

OY 11 ELAEYODLFTLKEOELLAHRRFCELLPOQRVTESSLRNOVPEQLS--LPELKNP 68
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 41 EGLEOLQOTFTKRELOVLYKGRFNECP-----SGIVNEENFKQIYSQFFPGDST 93
OY 69 FKERICRVSTSPAKDSIFEDFDLLSVFSDTATPDIKSHAFRIFDDGTLNRE-- 126
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 94 YATLEFNAPDTN-HDGSVFEDEVAGLSVIL-RGTVDRLMNAFNLYDLNKGCTIKREM 151
OY 127 -DLSRLVNCILGEGEDTRLASSEMKOLDNIIESDIDROGTINLSEFOHVISRSPDFAS 185
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 152 LDIMKSIYDMGKTYTPALREAPREHVESFQKMDRNKGDVVTIEEFIESCKDENIMR 211
OY 186 SFKI 189
| : :
DB 212 SMQL 215

```

RESULT 9

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US-09-350-874-20
; Sequence 20, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: NMI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-874-20

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```

Query Match      14.7%  Score 141;  DB 10;  Length 252;
Best Local Similarity 23.4%  Pred. No. 6.7e-07;
Matches 43;  Conservative 46;  Mismatches 81;  Indels 14;  Gaps 5;

```

```

OY 11 ELAEYODLFTLKEOELLAHRRFCELLPOQRVTESSLRNOVPEQLS--LPELKNP 68
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 73 EGLEOLQOTFTKRELOVLYKGRFNECP-----SGIVNEENFKQIYSQFFPGDST 125
OY 69 FKERICRVSTSPAKDSIFEDFDLLSVFSDTATPDIKSHAFRIFDDGTLNRE-- 126
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 126 YATLEFNAPDTN-HDGSVFEDEVAGLSVIL-RGTVDRLMNAFNLYDLNKGCTIKREM 183
OY 127 -DLSRLVNCILGEGEDTRLASSEMKOLDNIIESDIDROGTINLSEFOHVISRSPDFAS 185
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

DB 184 LDIMKSIYDMGKTYTPALREAPREHVESFQKMDRNKGDVVTIEEFIESCKDENIMR 243
OY 186 SFKI 189
| : :
DB 244 SMQL 247

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RESULT 10

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US-09-350-874-14
; Sequence 14, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: NMI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-874-14

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Query Match      14.7%  Score 141;  DB 10;  Length 270;
Best Local Similarity 23.4%  Pred. No. 7.4e-07;
Matches 43;  Conservative 46;  Mismatches 81;  Indels 14;  Gaps 5;

```

```

OY 11 ELAEYODLFTLKEOELLAHRRFCELLPOQRVTESSLRNOVPEQLS--LPELKNP 68
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 91 EGLEOLQOTFTKRELOVLYKGRFNECP-----SGIVNEENFKQIYSQFFPGDST 143
OY 69 FKERICRVSTSPAKDSIFEDFDLLSVFSDTATPDIKSHAFRIFDDGTLNRE-- 126
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 144 YATLEFNAPDTN-HDGSVFEDEVAGLSVIL-RGTVDRLMNAFNLYDLNKGCTIKREM 201
OY 127 -DLSRLVNCILGEGEDTRLASSEMKOLDNIIESDIDROGTINLSEFOHVISRSPDFAS 185
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 202 LDIMKSIYDMGKTYTPALREAPREHVESFQKMDRNKGDVVTIEEFIESCKDENIMR 261
OY 186 SFKI 189
| : :
DB 262 SMQL 265

```

RESULT 11

```

US-09-350-874-6
; Sequence 6, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: NMI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731

```

EARLIER FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 6
LENGTH: 216
TYPE: PRT
ORGANISM: Mus musculus
US-09-350-874-6

Query Match 14.3%; Score 138; DB 10; Length 216;
Best Local Similarity 25.6%; Pred. No. 1.1e-06;
Matches 43; Conservative 35; Mismatches 76; Indels 14; Gaps 5;

QY 11 ELAAYODLFTFKOEILLAHRRCELLPOEQRTVESLSRAQVFEQILS--LPELKAMP 68
DB 37 EGLEQLAQTNTFKRELQVLYRQFKNECP-----SGVNEEFKQIYAQFFPHGDAST 89
QY 69 FKERICVSTSPAKDSLEDFDLVSFSDTATPDIKSHYAFRIFDDGTLNREDL 128
DB 90 YAHYLFNAFTTQT-GSVKFEDEFYALSTLL-RGTVEKLRMTNLTNDKNGYINKEEM 147
QY 129 SRLVNC---LTGEGEDTRLASSEMQLIDNILEESDIDRGTINLSEF 173
DB 148 MDIVKAIYDMGKTYTPVLKEDTPRQHVDFQKMDKNKGIVTLDEF 195

RESULT 12

US-09-350-874-8
Sequence 8; Application US/09350874
Patent No. US20020019020A1
GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
APPLICANT: An, Wenqian
TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
FILE REFERENCE: MNI-069
CURRENT APPLICATION NUMBER: US/09/350,874
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: USSN 60/110,033
EARLIER FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: USSN 60/109,333
EARLIER FILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: USSN 09/298,731
EARLIER FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 8
LENGTH: 227
TYPE: PRT
ORGANISM: Rattus sp.
US-09-350-874-8

Query Match 14.3%; Score 138; DB 10; Length 227;
Best Local Similarity 25.6%; Pred. No. 1.2e-06;
Matches 43; Conservative 35; Mismatches 76; Indels 14; Gaps 5;

QY 11 ELAAYODLFTFKOEILLAHRRCELLPOEQRTVESLSRAQVFEQILS--LPELKAMP 68
DB 48 EGLEQLAQTNTFKRELQVLYRQFKNECP-----SGVNEEFKQIYAQFFPHGDAST 100
QY 69 FKERICVSTSPAKDSLEDFDLVSFSDTATPDIKSHYAFRIFDDGTLNREDL 128
DB 101 YAHYLFNAFTTQT-GSVKFEDEFYALSTLL-RGTVEKLRMTNLTNDKNGYINKEEM 158
QY 129 SRLVNC---LTGEGEDTRLASSEMQLIDNILEESDIDRGTINLSEF 173
DB 159 MDIVKAIYDMGKTYTPVLKEDTPRQHVDFQKMDKNKGIVTLDEF 206

RESULT 13
US-09-350-874-10
Sequence 10; Application US/09350874

Patent No. US20020019020A1
GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
APPLICANT: An, Wenqian
TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
FILE REFERENCE: MNI-069
CURRENT APPLICATION NUMBER: US/09/350,874
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: USSN 60/110,033
EARLIER FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: USSN 60/109,333
EARLIER FILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: USSN 09/298,731
EARLIER FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 10
LENGTH: 227
TYPE: PRT
ORGANISM: Mus musculus
US-09-350-874-10

Query Match 14.3%; Score 138; DB 10; Length 227;
Best Local Similarity 25.6%; Pred. No. 1.2e-06;
Matches 43; Conservative 35; Mismatches 76; Indels 14; Gaps 5;

QY 11 ELAAYODLFTFKOEILLAHRRCELLPOEQRTVESLSRAQVFEQILS--LPELKAMP 68
DB 48 EGLEQLAQTNTFKRELQVLYRQFKNECP-----SGVNEEFKQIYAQFFPHGDAST 100
QY 69 FKERICVSTSPAKDSLEDFDLVSFSDTATPDIKSHYAFRIFDDGTLNREDL 128
DB 101 YAHYLFNAFTTQT-GSVKFEDEFYALSTLL-RGTVEKLRMTNLTNDKNGYINKEEM 158
QY 129 SRLVNC---LTGEGEDTRLASSEMQLIDNILEESDIDRGTINLSEF 173
DB 159 MDIVKAIYDMGKTYTPVLKEDTPRQHVDFQKMDKNKGIVTLDEF 206

RESULT 14
US-09-350-874-4
Sequence 4; Application US/09350874
Patent No. US20020019020A1
GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
APPLICANT: An, Wenqian
TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
FILE REFERENCE: MNI-069
CURRENT APPLICATION NUMBER: US/09/350,874
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: USSN 60/110,033
EARLIER FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: USSN 60/109,333
EARLIER FILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: USSN 09/298,731
EARLIER FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 4
LENGTH: 245
TYPE: PRT
ORGANISM: Rattus sp.
US-09-350-874-4

Query Match 14.3%; Score 138; DB 10; Length 245;
Best Local Similarity 25.6%; Pred. No. 1.3e-06;
Matches 43; Conservative 35; Mismatches 76; Indels 14; Gaps 5;

QY 11 ELAAYODLFTFKOEILLAHRRCELLPOEQRTVESLSRAQVFEQILS--LPELKAMP 68

DB 66 EGELEQLEQTFKTRKELQVLYRGKNECP-----SGVNEETFKQIYAQFFPHGDAST 118
QY 69 FKERICAVFSTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHYAFRIEFDGDTLNREDL 128
DB 119 YAHFLFNAPFTQT- GSVKFEDEFYALSTILL- RGTVHEKLMFTNLVDINKDGYINKDEM 176
QY 129 SRLVNC---LTGEGEDTRLASSEMKOLIDNILESDDIDRGDTINLSEF 173
DB 177 MDIVKAIYDMGKXYTPYLKEDTPROHVDFVFOKKDKKDGIVTLDEF 224

RESULT 15

US-09-350-874-18
Sequence 18, Application US/09350874
Patent No. US20020019020A1
GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
TITLE OR INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
FILE REFERENCE: MNI-069
CURRENT APPLICATION NUMBER: US/09/350,874
CURRENT FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: USSN 60/110,033
EARLIER FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: USSN 60/109,333
EARLIER FILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: USSN 09/298,731
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 18
LENGTH: 270
TYPE: PRT
ORGANISM: Mus musculus
US-09-350-874-18

Query Match

14.3%; Score 138; DB 10; Length 270;

Best Local Similarity 25.0%; Pred. No. 1.5e-06;

Matches 42; Conservative 42; Mismatches 70; Indels 14; Gaps 5;

QY 11 ELAEYODLFLKQELLAHRRFCCLLPQEQRTVESLSRAOVPEQILS--LPRLKAMP 68
DB 91 EGLEQLQEQTKTRRREQLYRGKNECP-----SGVNEETFKQIYAQFFPHGDAST 143
QY 69 FKERICAVFSTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHYAFRIEFDGDTLNREDL 126
DB 144 YAHFLFNAPFTQT- HDGVSFEDEFYALSTILL- RGTIDRLNMAFNLYDLNKDGCITREEM 201
QY 127 -DLSRLVNCLEGTGEEDTRLASSEMKOLIDNILESDDIDRGDTINLSEF 173
DB 202 LDIKSTIYDMGKXYTPALREAPREHVESFQAMDRNKDGIVTLDEF 249

Search completed: November 21, 2002, 18:00:35
Job time: 12 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2002, 17:57:51 : Search time 35 seconds
(without alignments)
727.168 Million cell updates/sec

Title: US-09-878-454A-2

Perfect score: 962
Sequence: 1 MCGSGSRSLKELAEYODLT.....EFOHVYSRSPDASSKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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4:	/SID2/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:*
5:	/SID2/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT:*
6:	/SID2/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT:*
7:	/SID2/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT:*
8:	/SID2/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT:*
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22:	/SID2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
23:	/SID2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	958	99.6	191	19	AAW51215
2	952	99.0	191	19	AAW62287
3	950	98.8	191	19	AAW64199
4	379	39.4	172	22	AAU87324
5	379	39.4	184	22	AAW43562
6	377	39.2	185	22	AAW64418
7	362	37.6	173	22	ABW6054
8	362	37.6	173	22	AAU87612
9	362	37.6	173	22	AAW95362
10	362	37.6	173	22	AAW43637

11	362	37.6	173	22	AAU19952
12	345	35.9	187	22	AAE09736
13	343.5	35.7	206	22	ABW64325
14	244.5	25.4	169	23	ABW41194
15	220	22.9	120	20	AAU11976
16	204.5	21.3	175	20	AAU00881
17	195	20.3	175	20	AAU08118
18	195	20.3	210	21	AAU21177
19	194	20.2	175	21	AAU51586
20	194	20.2	175	23	ABW92357
21	192	20.0	175	21	AAU07824
22	186.5	19.4	170	19	AAW64200
23	186.5	19.4	170	21	AAW09787
24	185	19.2	169	21	AAU51587
25	183	19.0	169	22	AAU51587
26	182.5	19.0	189	22	ABW58936
27	181	18.8	169	21	AAU21179
28	176.5	18.3	187	22	ABW61857
29	176.5	18.3	187	22	ABW67063
30	175.5	18.2	162	22	ABW65554
31	174.5	18.1	170	22	ABW60493
32	170	17.7	170	21	AAU09977
33	170	17.7	170	22	AAU14411
34	170	17.7	173	22	AAW64410
35	170	17.7	187	22	AAU87327
36	170	17.7	189	22	ABW95336
37	170	17.7	189	22	AAU87615
38	170	17.7	189	22	AAW95339
39	170	17.7	189	22	AAW43564
40	170	17.7	189	22	AAW43639
41	170	17.7	189	22	AAU19951
42	164.5	17.1	226	21	AAU47032
43	163.5	17.0	226	21	AAU21163
44	157	16.3	190	21	AAU69996
45	156	16.2	194	22	AAU87585

ALIGNMENTS

RESULT 1

ID AAW51215 standard; Protein; 191 AA.

AAW51215;

21-AUG-1998 (first entry)

Amino acid sequence of the calcium-integrin binding protein.

Human calcium-integrin binding protein; CIB; Integrin alpha IIB; Cytoplasmic domain; platelet; alpha IIB-beta-3; fibrinogen receptor; Inhibition; blood coagulation; vascular disorder.

Homo sapiens.

Key

Region

Region

Region

Region

Region

Region

Region

Region

Region

Region

Region

Region

Novel human calcinu
Human kinase inter
Drosophila melanog
Human ovarian anti
Human 5' EST seque
Calcineurin regula
Zea mays protein f
Zea mays protein f
Arabidopsis thalia
Herbicidally activ
Arabidopsis thalia
Human calcineurin.
Human HCNB protein
Arabidopsis thalia
Arabidopsis thalia
Drosophila melanog
Zea mays protein f
Drosophila melanog
Drosophila melanog
Drosophila melanog
Human CNBII protel
Calcineurin B subu
Amino acid sequenc
Novel central nerv
Human testicular a
Novel central nerv
Human reproductive
Human polypeptide
Novel human calcin
Arabidopsis thalia
Arabidopsis thalia
Human receptor-ass
Novel central nerv

XX WPI; 1998-240018/21.
 DR N-PSDB; AAV07211.
 XX
 PT New isolated calcium-integrin binding protein - is expressed in
 PT platelets and activates the fibrinogen receptor. used to develop
 PT products for treating e.g. vascular disorders
 XX
 PS Claim 1: Page 30; 44pp; English.
 CC This is the amino acid sequence of the human calcium-integrin binding
 CC (CIB) protein, that binds to the integrin alpha IIB cytoplasmic
 CC domain. The CIB protein is expressed in platelets and interacts with
 CC the alpha IIB subunit of integrin alpha IIB- beta 3, to activate the
 CC fibrinogen receptor. Inhibitory compounds where it is desired to inhibit the
 CC activation of the fibrinogen receptor where it is desired to reduce
 CC blood coagulation for therapeutic, diagnostic or pharmaceutical
 CC reasons. The products can be used for treating vascular disorders,
 CC and for isolating or purifying integrins or fibrinogen. They can also
 CC be used for detection and diagnosis.
 CC
 XX
 SQ Sequence 191 AA:
 Query Match 99.6%; Score 958; DB 19; Length 191;
 Best Local Similarity 99.5%; Pred. No. 3.3e-93;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSGSRLSKELAEYODLFTLKQETLLAHRFCCELLPOQRVSSSLRAQVPEQILS 60
 DB 1 MGSGSRLSKELAEYODLFTLKQETLLAHRFCCELLPOQRVSSSLRAQVPEQILS 60
 QY 61 LPELKANPFKERICRVSTSPAKDSLSFEDFLDLVSFSDTAPDIKSHYAFRIFFDDDD 120
 DB 61 LPELKANPFKERICRVSTSPAKDSLSFEDFLDLVSFSDTAPDIKSHYAFRIFFDDDD 120
 QY 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKQIDNIEESDIDRDGTINLSEFOHVISRS 180
 DB 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKQIDNIEESDIDRDGTINLSEFOHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191
 RESULT 2
 ID AAM62287 standard; Protein; 191 AA.
 XX
 AC AAM62287;
 XX
 DT 24-SEP-1998 (first entry)
 XX
 DE Human protein phosphatase regulatory subunit.
 XX
 KW Human; protein phosphatase regulatory subunit; HCNB; diagnosis;
 KW immunosuppression; neurodegeneration; inflammation; cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 44 /label= unknown
 FT /note= "encoded by ASC"
 FT Misc-difference 45 /label= unknown
 FT /note= "encoded by TGN"
 XX
 PN MO9826056-A1.
 XX
 PD 18-JUN-1998.
 XX
 PE 25-NOV-1997; 97WO-US21603.
 XX

PR 12-DEC-1996; 960S-0764563.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Goll SK, Hillman JL;
 XX
 DR WPI; 1998-348518/30.
 DR N-PSDB; V398009.
 XX
 PT New protein phosphatase regulatory sub-unit - useful for diagnosis,
 PT prevention and treatment of immuno-suppression, neuro-degeneration,
 PT inflammation and cancer
 XX
 PS Claim 1: Fig 1; 65pp; English.
 CC The present sequence is a pure human protein phosphatase regulatory
 CC subunit (HCNB). Host cells, comprising a vector containing DNA encoding
 CC HCNB, are used to produce recombinant HCNB which is used to treat or
 CC prevent immunosuppression or neurological diseases (especially parasitic,
 CC bacterial or viral infections, including AIDS; the effects of radio- or
 CC chemo-therapy and Alzheimer's disease). Antagonists which bind
 CC specifically to HCNB and modulate its activity are used to treat
 CC inflammation, cancer, or immunological disorders and allograft rejection
 CC (especially anaemia, asthma, systemic lupus erythematosus, myasthenia
 CC gravis, diabetes, thyroiditis, ulcerative colitis, osteoporosis and
 CC arthritis). Complements of the DNA encoding HCNB are useful as probes
 CC and primers for detecting the DNA encoding HCNB by hybridisation or
 CC amplification assays, while Ab can be used to detect HCNB by immunoassay,
 CC particularly for diagnosis of the specified disorders, including early
 CC diagnosis of cancers. The probes can also be used to map the
 CC corresponding genomic sequence, while Ab are also useful in drug
 CC screening and for purifying native HCNB. Therapeutic agents are
 CC administered orally, intravenously, intramuscularly, topically or
 CC rectally, normally at 0.1-105 mg g.
 XX
 SQ Sequence 191 AA:
 Query Match 99.0%; Score 952; DB 19; Length 191;
 Best Local Similarity 99.0%; Pred. No. 1.4e-92;
 Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MGSGSRLSKELAEYODLFTLKQETLLAHRFCCELLPOQRVSSSLRAQVPEQILS 60
 DB 1 MGSGSRLSKELAEYODLFTLKQETLLAHRFCCELLPOQRVSSSLRAQVPEQILS 60
 QY 61 LPELKANPFKERICRVSTSPAKDSLSFEDFLDLVSFSDTAPDIKSHYAFRIFFDDDD 120
 DB 61 LPELKANPFKERICRVSTSPAKDSLSFEDFLDLVSFSDTAPDIKSHYAFRIFFDDDD 120
 QY 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKQIDNIEESDIDRDGTINLSEFOHVISRS 180
 DB 121 GTLNREDLSRLVNCITGEGEDTRLASASEMKQIDNIEESDIDRDGTINLSEFOHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191
 RESULT 3
 ID AAM64199 standard; Protein; 191 AA.
 XX
 AC AAM64199;
 XX
 DT 09-NOV-1998 (first entry)
 XX
 DE Human interferon receptor 1 binding protein IR1B1.
 XX
 KW Interferon receptor 1 binding protein; IR1B1; human; tumour;
 KW cancer; gene therapy; tissue graft; graft survival.
 XX
 OS Homo sapiens.
 XX

PN WO9831796-A1.
 XX 23-JUL-1998.
 XX 15-JAN-1998; 98WO-US00671.
 XX 15-JAN-1997; 97US-0035636.
 XX (MCIN/) MCINNIS P A.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX Adramovitch C, Chebath JE, Revel M;
 XX MPI: 1998-414096/35.
 DR N-PSDB; AAV44272.
 XX
 PT New isolated interferon receptor binding proteins - used to develop
 PT products for modulating sensitivity to interferon, e.g. in the
 PT treatment of tumours or for prolonging graft survival
 XX
 PS Claim 1: Page 34; 64pp: English.

CC This is a novel human protein, designated interferon receptor
 CC binding protein 1 (IRB1), which interacts with the intracytoplasmic
 CC (IC) domain of the IFNAR1 chain of the interferon type I (IFN-alpha,
 CC beta or omega) receptor. IRB1 is a new member of the calcineurin
 CC and calcitricin family of calcium-regulated proteins (see also
 CC AAM64200). It is induced very rapidly and transiently following IFN
 CC treatment of human cells. It was identified in a two-hybrid
 CC screening for proteins interacting with the IFNAR1-IC domain;
 CC another protein, IRB4 (see AAM64202), was similarly identified. A
 CC cDNA clone (see AAV44272) encoding IRB1, host cells and expression
 CC vectors are claimed. DNA encoding IRB1, and IRB4 can be used in
 CC cancer therapy where the increased cellular response to IFN would
 CC result in a decrease in malignant cell growth and an enhanced
 CC response to exogenous IFN therapy. Antisense IRB1 or IRB4
 CC nucleic acids can be used for prolonging tissue or organ graft
 CC survival in patients as the rejection of these grafts in the host
 CC is mediated by the histocompatibility antigens (MHC class I) whose
 CC synthesis depends on the IFN stimulus. The products can also be
 CC used in detection and diagnosis.

CC Sequence 191 AA;

Query Match 98.8%; Score 950; DB 19; Length 191;
 Best Local Similarity 99.0%; Pred. No. 2,3e-92;

Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSGSRLSKELAEYQDLFLTKOELLAHRRFCCLPEORTVSSSLAAQVPEIDLS 60
 DB 1 MGSGSRLSKELAEYQDLFLTKOELLAHRRFCCLPEORTVSSSLAAQVPEIDLS 60
 QY 61 LPELKNPKEKICRVFSTSPANDSLSFEDFLDLVSFSTPATPKSHAFRIFEDDD 120
 DB 61 LPELKNPKEKICRVFSTSPANDSLSFEDFLDLVSFSTPATPKSHAFRIFEDDD 120
 QY 121 GTINRDLISRLVNCITGEEBDRILASSEKQIDLTNLESDDIDRGTINLSEFOHVISRS 180
 DB 121 GTINRDLISRLVNCITGEEBDRILASSEKQIDLTNLESDDIDRGTINLSEFOHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 4
 AAU87324
 ID AAU87324 standard; Protein; 172 AA.
 XX AAU87324;
 AC
 XX
 DT 05-JUN-2002 (first entry)
 XX

DE Novel central nervous system protein #234.
 XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy.
 XX Homo sapiens.
 OS
 XX
 PN WO200155318-A2.
 XX
 PD 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US01332.
 XX
 PF 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0225779.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226688.
 PR 22-AUG-2000; 2000US-0227009.
 PR 23-AUG-2000; 2000US-0227182.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0231242.
 PR 05-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231423.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.

PR	05-DEC-2000;	2000US-0251030.			
PR	05-DEC-2000;	2000US-0251988.			
PR	05-DEC-2000;	2000US-0256719.			
PR	06-DEC-2000;	2000US-0251479.			
PR	08-DEC-2000;	2000US-0251856.			
PR	08-DEC-2000;	2000US-0251868.			
PR	08-DEC-2000;	2000US-0251869.			
PR	08-DEC-2000;	2000US-0251989.			
PR	11-DEC-2000;	2000US-0251990.			
PR	11-DEC-2000;	2000US-0254097.			
XX	05-JAN-2001;	2001US-0259678.			
PA	(HUMA-) HUMAN GENOME SCI INC.				
XX					
PI	Rosen CA, Barash SC, Ruben SM;				
XX					
DR	WPI: 2001-581633/65.				
NR	N-PDSB: ABAK3654.				
PT	New isolated nucleic acid encoding a protein for diagnosing,				
PT	preventing, treating or ameliorating medical conditions and used as				
PT	food additives or preservatives -				
XX					
PS	Claim 9; SEQ ID NO 842; 837pp; English.				
XX					
CC	The invention describes an isolated nucleic acid molecule (I) encoding a				
CC	novel central nervous system protein. (I) and polypeptides (II) encoded				
CC	by (I), are used to treat a medical conditions and in diagnosis of a				
CC	pathological condition. Disorders which are diagnosed or treated include				
CC	autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative				
CC	disorders e.g. neoplasms of the breast or liver, cardiovascular disorders				
CC	e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,				
CC	angiogenesis, nervous system disorders e.g. Alzheimer's disease and				
CC	amyotrophic lateral sclerosis, infections caused by bacteria, viruses				
CC	e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders				
CC	e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,				
CC	adenocarcinomas and irritable bowel syndrome, reproductive system				
CC	disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes				
CC	and pituitary dwarfism, cancers and disorders at the cellular level e.g.				
CC	leukaemia, disorders involving neovascularisation e.g. malignancies,				
CC	respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.				
CC	acute kidney failure and blood related disorders e.g. myocardial				
CC	infarction. The polypeptides can also be used to aid wound healing and				
CC	epithelial cell proliferation, to prevent skin aging due to sunburn, to				
CC	maintain organs before transplantation, for supporting cell culture of				
CC	primary tissues, to regenerate tissues and in chemotaxis. The				
CC	polypeptides can also be used as a food additive or preservative to				
CC	increase or decrease storage capabilities, fat content, lipid, protein,				
CC					
Query Match	39.4%; Score 379; DB 22; Length 172;				
Best Local Similarity	44.1%; Pred. No.5-6e-32;				
Matches	78; Conservative	36; Mismatches	53; Indels	10; Gaps	3
OY	13 LAEVDLTLFKQELLHAHRFCELLPOEQRTVESSLRAQVPEOILSLPELKANPFKER	72			
DB	1 LEEYQATFLFNELTICHTDFTLCKCPKKYYKEIT---TMDQVSIPALRVNPFDR	56			
OY	73 ICRVSTSPARDLSFEFDLDLSVFSQATPDTSHTYAFRFPDDSDOSTLRKEDLSRY	132			
DB	57 ICRVYS---HKMFSEFDVLGMAVSFSDACSLTEIAFRFYDENENEFIDEEDLRII	113			
OY	133 NCLTGEGETRLSASEMKOLINDILEESIDIDRGCTINISLEFOHVISRSPDFASSERI	189			
DB	114 LRLLNSDD---MSEDLIDLTHIVLSSESDLDNDMLSFSEFHAAKSPDFMANSERI	167			
RESULT 5					
ID	AAM43562				
NC	AAM43562 standard; Protein: 184 AA.				
XX	AAM43562;				
DT	22-OCT-2001 (first entry)				

05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-488781/53.
 DR N-PSDB; AAF63868.
 XX
 PT New isolated nucleic acids and polypeptides, useful for diagnosing,
 PT treating and/or preventing human diseases and disorders.
 XX
 PS Claim 11; SEQ ID NO 240; 664pp + Sequence Listing; English.
 CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
 CC the encoded proteins (AAI64497-AAI64660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 184 AA;
 Query Match 39.4%; Score 379; DB 22; Length 184;
 Best Local Similarity 44.1%; Pred. No. 6.2e-32;
 Matches 78; Conservative 36; Mismatches 53; Indels 10; Gaps 3;
 QY 13 LAEYQDLFTFKQKELLNHRRCCELLPQQRVSSLRQVPEQILSLPELKANPKER 72
 DB 13 LEEYQALFTLRNEILCHDIFLKCPGKYYKEATL---TMDVSSLPALRVNPPDR 68
 QY 73 ICRVSTSPANDSLSEDFDLVSFSDTAPDPIKSHYAFRIEDDDGTLNREDLSRV 132
 DB 69 ICRVFS---HKGMFSEFDVLGNASVSEQACSLKIEYAFRIYDENGFIDEDLQRT 125
 QY 133 NCLTGEEDTRLASAKMQLINDIIEESDIDRGTINLSEFOHVISRSPFASSTKI 189
 DB 126 LRLINSD---WSEDLMDLTNHLVLSSEDLNDNMLSFSEFEHAKMSPDFMSPRI 179
 RESULT 6
 AAB64418
 ID AAB64418 standard; Protein; 185 AA.
 AC AAB64418;
 XX
 DE 22-MAR-2001 (first entry)
 XX
 DE Amino acid sequence of human intracellular signalling molecule INTRA50.
 XX
 KW Human; intracellular signalling molecule; INTRA; immunosuppressive;
 KW cytostatic; neuroprotective; nootropic; antiarteriosclerotic; cancer;
 KW antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;

antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
 KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
 KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
 KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
 KW mental disorder; schizophrenia; anxiety.
 XX
 OS Homo sapiens.
 XX
 PN WO200077040-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 16-JUN-2000; 2000WO-US16636.
 XX
 PR 16-JUN-1999; 99US-0139566.
 PR 17-AUG-1999; 99US-0146640.
 PR 09-NOV-1999; 99US-0164417.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Yue H, Tang YT, Hallman JL, Lal P, Bandman O, Baughn MR;
 PI Azimzai Y, Yang J, Reddy R, Lu DM;
 XX
 DR WPI: 2001-025334/03.
 DR N-PSDB; AAF32687.
 XX
 PT New human intracellular signalling molecules, useful for the diagnosis,
 PT prevention and treatment of cell proliferative, autoimmune,
 PT inflammatory, neurological, gastrointestinal, reproductive and
 PT developmental disorders.
 XX
 PS Claim 5; Page 158-159; 192pp; English.
 CC Sequences AAF32638 - AAF32689 represent cDNA encoding human
 CC intracellular signalling molecules INTRA1 - INTRA52, represented in
 CC AAB64369 - AAB64420. Modulators of the intracellular signalling molecules
 CC of the invention exhibit immunosuppressive; cytostatic; neuroprotective;
 CC nootropic; antiarteriosclerotic; antiinflammatory; anti-HIV;
 CC neuroleptic; antibacterial; antifungal; antiviral; antiparasitic;
 CC antihelminthic; and antiparkinsonian activity. INTRA polypeptides their
 CC agonists and antagonists are useful for the treatment of a condition
 CC associated with decreased or increased expression of functional INTRA.
 CC Disorders associated with abnormal INTRA expression or activity include
 CC cell proliferative disorders e.g. arteriosclerosis and cancers;
 CC autoimmune or inflammatory disorders e.g. Addison's disease and acquired
 CC immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,
 CC protozoal and helminthic infections; gastrointestinal disorders e.g.
 CC dysphagia and irritable bowel syndrome; neurological disorders e.g.
 CC epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob
 CC disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
 CC disorder. Antibodies immunospecific for the INTRA proteins may also be
 CC useful in the diagnosis of the above disorders.
 XX
 SQ Sequence 185 AA;
 Query Match 39.2%; Score 377; DB 22; Length 185;
 Best Local Similarity 44.1%; Pred. No. 1e-31;
 Matches 79; Conservative 35; Mismatches 55; Indels 10; Gaps 3;
 QY 11 ELAEYQDLFTFKQKELLNHRRCCELLPQQRVSSLRQVPEQILSLPELKANPK 70
 DB 12 LEEYQALFTLRNEILCHDIFLKCPGKYYKEATL---TMDVSSLPALRVNPPDR 67
 QY 71 ICRVSTSPANDSLSEDFDLVSFSDTAPDPIKSHYAFRIEDDDGTLNREDLSRV 130
 DB 68 ICRVFS---HKGMFSEFDVLGNASVSEQACSLKIEYAFRIYDENGFIDEDLQRT 124
 QY 131 NCLTGEEDTRLASAKMQLINDIIEESDIDRGTINLSEFOHVISRSPFASSTKI 189
 DB 125 IIRLINSD---WSEDLMDLTNHLVLSSEDLNDNMLSFSEFEHAKMSPDFMSPRI 180
 RESULT 7

AB96054
ID AB96054 standard; Protein; 173 AA.
XX
AC AB96054;
XX
DT 21-JUN-2002 (first entry)
XX
DE Human testicular antigen SEQ ID NO: 1438.
XX
KW Human: testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic.
OS Homo sapiens.
XX
PN W0200155317-A2.
XX
PD 02-AUG-2001.
XX
PE 17-JAN-2001; 2001WO-US01329.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229309.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
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PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
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PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.

PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben EM;
XX WPI; 2001-483232/52.
XX
XX Nucleic acids encoding 973 human testicular antigen polypeptides,
XX useful for preventing, diagnosing and/or treating testicular cancer -
XX
XX Claim 11; SEQ ID NO 1438; 766bp; English.
XX
XX The present invention provides the protein and coding sequences of 973
XX human testicular antigens, and fragments of their genomic sequences. The
XX sequences can be used in the treatment of cardiovascular, urinary system,
XX reproductive system, immune, respiratory, neurological and
XX gastrointestinal disorders, infections, and particularly cancer,
XX especially testicular cancers. The present sequence is a protein of the
XX invention.
XX
XX Sequence 173 AA;
XX
XX Query Match 37.6%; Score 362; DB 22; Length 173;
XX Best Local Similarity 42.9%; Pred. No. 3.6e-30;
XX Matches 75; Conservative 35; Mismatches 55; Indels 10; Gaps 3;
XX
XX 13 LAEVDLFLKQETLHARRFCELPQERTVSSLAQVFPFQIISLPKANKPER 72
XX 1 LEEVQALFLTRNELICHTDFLKCPGKYKENTL---TMOQVSLPLRVNPFDR 56
XX
XX 73 ICRVFTSPKADSLSEDFDLILSVFSDPATPIKSHYAFRIFFDDGTINREDLSRLV 132
XX 57 ICRVFS---HKGMSEFDEVLGMASVSEQACPSLKIEAFRIYDFENGFIDEEDLORII 113
XX
XX 133 NCLGEGEDTRLSASEMKQLIDNIIIESDIDRDGTINSEFOHYISRPDFASSF 187
XX 114 LRLNSDD---MSEDLIMDLTNHVLXSKSLDNDNMLSPSEFEHMAKSPDEMTPE 165
XX
XX RESULT 8
XX AA087612
XX ID AA087612 standard; Protein; 173 AA.
XX
XX AA087612;
XX
XX 05-JUN-2002 (first entry)
XX
XX Novel central nervous system protein #522.
XX
XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;
XX cardiac arrest; cerebrovascular disorder; ischemia; angioneu-
XX rous system disorder; Alzheimer's disease; AIDS; ocular disorder;
XX acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
XX adenocarcinoma; reproductive system disorder; testicular feminization;
XX endocrine disorder; diabetes; cancer; leukemia; neovascularization;
XX respiratory disorder; renal disorder; kidney failure; blood disorder;
XX myocardial infarction; wound healing; cell proliferation; skin aging;
XX food additive; food preservative; gene therapy.
XX
XX Homo sapiens.
XX
XX OS

XX
XX PN WO200155318-A2.
XX XX
XX PD 02-AUG-2001.
XX
XX PE 17-JAN-2001; 2001WO-US01332.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 02-MAR-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
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XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217486.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
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XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
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XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
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XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
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XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
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XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
XX 14-SEP-2000; 2000US-0232398.
XX 14-SEP-2000; 2000US-0232399.
XX 14-SEP-2000; 2000US-0232400.
XX 14-SEP-2000; 2000US-0232401.
XX 14-SEP-2000; 2000US-0233063.
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XX 25-SEP-2000; 2000US-0234988.
XX 26-SEP-2000; 2000US-0235484.
XX 27-SEP-2000; 2000US-0235834.
XX

PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
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 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
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 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241851.
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 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
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 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
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 PR 08-NOV-2000; 2000US-0246609.
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 PR 17-NOV-2000; 2000US-0249207.
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 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
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 PR 01-DEC-2000; 2000US-0250160.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 03-JAN-2001; 2001US-0259678.
 XX
 XX
 (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX

PI Rosen CA, Barash SC, Ruben SM;
 XX WPI: 2001-581633/65.
 DR N-PSDB; ABK43942.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX
 PS Claim 9; SEQ ID NO 1130; 837pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (II) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC
 Query Match 37.6%; Score 362; DB 22; Length 173;
 Best Local Similarity 42.9%; Pred. No. 3; 6e-30;
 Matches 75; Conservative 35; Mismatches 55; Indels 10; Gaps 3;
 QY 13 LAEYQDLFTFKQELILAHRCFELLPQEQRTVESSIRAOVPEQILSEELKMPKER 72
 Db 1 LEEYQALFTPLRNEICIDHDTFLKCPGKYKEATL---TMDQVSLPALRVNPPRDR 56
 QY 73 ICRVFTSPAKDSLSPFEDLILSVFSDTATPDIKSKYARIRPDDGTLNRDLSRLV 132
 Db 57 ICRVFTSPAKDSLSPFEDLILSVFSDTATPDIKSKYARIRPDDGTLNRDLSRLV 132
 QY 133 NCLTGGEDTRLASAEKQIDNILESDIDRDGTINLSEFOHYISRPDPASGF 187
 Db 114 LRLNSDD--NSEDLLMDLTNHYLSKSDLDNMLSFSEFHAMAKSPDMPMF 165
 RESULT 9
 AAM95362
 ID AAM95362 standard; Protein; 173 AA.
 XX
 AC AAM95362;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Human reproductive system related antigen SEQ ID NO: 4020.
 XX
 KW Human; reproductive system related antigen; reproductive system disorder;
 KW cancer; gene therapy.
 OS Homo sapiens.
 OS
 OS WO200155320-A2.
 PN
 XX 02-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US01339.
 PF
 XX

PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
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PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
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PR 23-AUG-2000; 2000US-0227009.
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PR 05-SEP-2000; 2000US-0229509.
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PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0232080.
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PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241786.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
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PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
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PR 17-NOV-2000; 2000US-0249215.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249263.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251477.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA
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XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465570/50.
XX N-PSDB; AAL01332.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen
is used in preventing, treating or ameliorating a medical condition

XX Claim 11; SEQ ID NO 4020; 1297pp + Sequence Listing; English.
PS
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention.
XX
SQ Sequence 173 AA;

Query Match 37.6%; Score 362; DB 22; Length 173;
Best Local Similarity 42.9%; Pred. No. 3,6e-30;
Matches 75; Conservative 35; Mismatches 55; Indels 10; Gaps 3;

QY 13 LAEYODTFLTKOELLAHRRPCELLPQEQRYVSSLAQVPPQILSLKLANPKER 72
DB 1 LEEYQALFLTRNELLICHTFELKLCPPKRYKEATL---TMDQVSSLALRVNPPRDR 56
QY 73 ICRVFTSPAKDSLSEDFELDLVSFSDTATPDIKSHYAFRIFDQDDGTINRDLRLV 132
DB 57 ICRVFS---HKMFSPEDVIGMASVSEQACPSIKETAFRITDFENGFIDEEDLQRTI 113
QY 133 NCLTGEEDTRLASAEKKOLIDILESDIDRDGTINLSEFOHYISNPPFASF 187
DB 114 LRLINSD--MSEDLMLDLTNHVLKSLDLNDNMLSFSEFEHMAKSPDPMTPF 165

RESULT 10
AAM43637
ID AAM43637 standard; Protein; 173 AA.
XX
AC AAM43637;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 315.
XX
KW Human; antitachytic; antipneumatic; antiproliferative; vasotropic;
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; vitucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; neurotropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; vulnery; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX
PN WO200155308-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01309.
XX
PR 31-JAN-2000; 2000US-0179065.
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PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0218290.
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PR 14-AUG-2000; 2000US-0225213.
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PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0228099.
PR 01-SEP-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234597.
PR 25-SEP-2000; 2000US-0234598.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236602.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239835.
PR 13-OCT-2000; 2000US-0239837.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.

PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246533.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
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 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-488781/53.
 DR N-PSDB; AAI63943.
 XX
 PT New isolated nucleic acids and polypeptides, useful for diagnosing,
 PT treating and/or preventing human diseases and disorders -
 XX
 PS Claim 11; SEQ ID NO 315; 664pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
 CC the encoded proteins (AAI634497-AAI63660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 173 AA:
 Query Match 37.6%; Score 362; DB 22; Length 173;
 Best Local Similarity 42.9%; Pred. No. 3,6e-30;
 Matches 75; Conservative 35; Mismatches 55; Indels 10; Gaps 3;
 OY 13 LAEYDPLFETQKQETLLARRCCCLLPQORVVESSLRAQVPEQLSLPELKANFKER 72
 DB 1 LEEYQALFFLLNKEILCHDFLKCPGKYKEATL---TWQVSSLPALRVNPFRR 56
 OY 73 ICRVFTSPAKDLSFEDELFLSVFSDTATPDIKSHVAFRTFDDDTLNRDLRSRV 132
 DB 57 ICRVFS---HKGMFSEFDVLGMASVSEQACPSIKETVAFRTYDFNENGFIDEEDQRII 113
 OY 133 NCLTGEEDTRISASEMKOLINILEESDIDPDGNTINLSEFOVIRSFPDFASSF 187
 DB 114 IRLNLSDD---MSEDLMLDTNHLVLSXSDLDNDNMLSEFEFERAMAKSPDFTMP 165
 RESULT 11
 AAU19952
 ID AAU19952 standard; Protein; 173 AA.
 XX
 AC AAU19952;
 XX
 DT 06-DEC-2001 (first entry)
 XX
 DE Novel human calcium-binding protein #61.
 XX
 KW Human: calcium-binding protein; calcium flux; neurological disease;
 KW immune dysfunction; digestive disorder; neoplastic disease;
 KW blood disorder; infectious disease; gene therapy; immunosuppressive;
 KW antithrillitic; cytostatic; vasotropic; antibacterial; nootropic;
 KW virucide.
 XX
 OS Homo sapiens.
 XX
 PN WO20015304-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01302.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
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 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0218880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 12-SEP-2000; 2000US-0232081.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 25-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
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 PR 02-OCT-2000; 2000US-0237038.
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 PR 13-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239835.
 PR 20-OCT-2000; 2000US-0239837.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251899.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-465568/50.

DR N-PSDB; AAS31637.

PT Isolated nucleic acid molecule encoding a calcium-binding protein is
 XX used in preventing, treating or ameliorating a medical condition -
 PS Claim 11; SEQ ID NO 149; 542pp; English.

XX The present invention relates to the isolation of novel human
 CC calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
 CC sequences encoding for these proteins. The sequences of the invention
 CC are useful in the diagnosis, prevention and/or prognosis of diseases
 CC associated with aberrant calcium flux. Such disorders include
 CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
 CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),
 CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
 CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
 CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
 CC novel calcium-binding proteins are also useful as screening tools to
 CC identify antagonists and/or agonists that may enhance or inhibit
 CC activities mediated by calcium-binding proteins. The polynucleotides of
 CC the invention are also useful in gene therapy. AAV19892-AAV19969
 CC represent the novel human calcium-binding proteins.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX

Sequence 173 AA;

Query Match 37.6%; Score 362; DB 22; Length 173;
 Best Local Similarity 42.9%; Pred. No. 3.6e-30;
 Matches 75; Conservative 35; Mismatches 55; Indels 10; Gaps 3;

QY 13 LAEYQDTFLTKQELILAHRRFCCELLPOEQRTVSSLRACVPEQQLISLPKLANPFRER 72
 DB 1 LEEYQALTFETLRNEIICIHDTFLKCPGKYKEATL---TWQYSSLPALRVNPPRDR 56
 QY 73 ICVFSTSPAKDSLFEDFLDLSVSDTTPRIKSHYARIPDPDDGLNEDLSRLV 132
 DB 57 ICVFSTSPAKDSLFEDFLDLSVSDTTPRIKSHYARIPDPDDGLNEDLSRLV 132
 QY 133 NCTGCEGDEPTRLSASEMKOLINDILESDIDRDGTINLSEFOHVISRPPFASSE 187
 DB 114 LRLNSDD---MSEDLMDLTNHYLSKSDLDNDNMLSFSEFEHAKKSPDFMTPF 165
 RESULT 12
 ID AAE09736 standard; protein; 187 AA.
 AC AAE09736;
 DT 29-NOV-2001 (first entry)
 DE Human kinase interacting protein.
 KW Human; kinase interacting protein; novel human protein; NHP;
 KW gene therapy; drug screening; mental disorder; biological disorder;
 KW medical disease; nootropic.
 OS Homo sapiens.
 XX
 PN WO200166760-A2.
 PD 13-SEP-2001.
 PF 08-MAR-2001; 2001WO-US07499.
 PR 08-MAR-2000; 2000US-0187719.
 PA (LEXI-) LEXICON GENETICS INC.
 PI Mathur B, Turner CA;
 PI WPI, 2001-557870/62.
 DR N-PSDB; AAD16796.
 XX
 PT Novel polynucleotides encoding human kinase interacting protein useful
 PT for drug screening, diagnosis and in gene therapy of biological
 PT disorders -
 PS Claim 2; Page 31-32; 32pp; English.
 CC The present amino acid sequence is a novel human protein (NHP),
 CC human kinase interacting protein. NHP oligonucleotides are useful
 CC as hybridization probes for screening libraries and assessing gene
 CC expression patterns. Sequences derived from regions adjacent to the
 CC intron/exon boundaries of NHP gene are used to design primers for
 CC use in amplification assays to detect mutations within the exons,
 CC splice sites, introns that can be used in diagnostics and
 CC pharmacogenomics. NHP nucleotide sequences are useful for drug
 CC screening and nucleotide construct encoding NHP products are
 CC useful in gene therapy for modulating NHP expression and to produce
 CC genetically engineered host cells to express NHP products in vivo.
 CC The encoded NHP polypeptides are useful for generating antibodies,
 CC as reagents in diagnostic assays, for identifying other cellular
 CC gene products related to NHP and as reagents in assays for screening
 CC for compounds that are useful in the treatment of mental, biological
 CC or medical disorders and diseases.
 CC
 SQ Sequence 187 AA;

Query Match 35.9%; Score 345; DB 22; Length 187;
 Best Local Similarity 40.4%; Pred. No. 2.5e-28;
 Matches 78; Conservative 42; Mismatches 61; Indels 12; Gaps 5;

QY 1 MGGSGSRLSKELLAEOYDITFLTKQELILAHRRFCCELLPO---EORTVSSLRACVPE 56
 DB 1 MGGSGSRLSKELLAEOYDITFLTKQELILAHRRFCCELLPO---EORTVSSLRACVPE 56
 QY 57 QIISLPKLANPFRERICRVSSTSPAKDSLFEDFLDLSVSDTTPRIKSHYARIP 116
 DB 58 LIOSMPELKNPFRERICRVSSTSPAKDSLFEDFLDLSVSDTTPRIKSHYARIP 116
 QY 117 FDDGDTNLRNEDLSRLVNCLEGEDEPTRLSASEMKOLINDILESDIDRDGTINLSEFOH 176
 DB 117 FDDGDTNLRNEDLSRLVNCLEGEDEPTRLSASEMKOLINDILESDIDRDGTINLSEFOH 176
 QY 177 ISRSPDFASSFKI 189
 DB 173 ILRAPDFLSTFHI 185
 RESULT 13
 ID ABB64325 standard; protein; 206 AA.
 AC ABB64325;
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 19767.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PF 23-MAR-2001; 2001WO-US09231.
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PA (PEKE) PE CORP NY.
 PI Venter JC, Adams M, Li PMD, Myers EW;
 PI WPI, 2001-656860/75.
 DR N-PSDB; ABL08428.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Disclosure; SEQ ID NO 19767; 21pp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB116175) and the encoded proteins
 CC (AB057737-AB072072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.
 CC
 SQ Sequence 206 AA;

Query Match 35.7%; Score 343.5; DB 22; Length 206;
 Best Local Similarity 44.3%; Pred. No. 4.1e-28;
 Matches 78; Conservative 30; Mismatches 51; Indels 17; Gaps 5;
 QY 17 QDITFLTKQELILAHRRFCCELLPO---EORTVSSLRACVPEQQLISLPKLANPFRER 73

Db 43 KDCFTFRKRLVHKKRRLRDLVPRQWTEGQASSVKKPCCEIKMPELR-----94
 QY 74 CRFESFSPAKDSLSEDFDLVSFSDTTPDIKSHYAFRFPDDGTLNRDLSRLVN 133
 Db 95 -ENAFSD--GQGNLSFEDFDLALSVFSEQAPRKIVYAFKRYDPDDGFIGHDA--LMS 149
 QY 134 CLTGEEDTRLASSEKOLIDNLEESDIDRGTINLSEFQHYISRPDFASSF 169
 Db 150 CLTWTMRN-ELSPFEHQIADKYIEADVDGDKLSLFEFHVILRPDLSTFHI 204
 RESULT 14
 ID ABP41194 standard; protein; 169 AA.
 AC ABP41194;
 DT 23-AUG-2002 (first entry)
 DE Human ovarian antigen HTLN94, SEQ ID NO:2326.
 XX
 KY Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KM ovarian cancer; breast cancer; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KM PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KM cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KM gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KM antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US18569.
 XX
 PR 07-JUN-2000; 2000US-209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI: 2002-147878/19.
 XX
 DR N-PSDB; AB054271.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.
 PT ovarian cancer), immune disorders, cardiovascular disorders and
 PT neurological diseases -
 XX
 PS Claim 11; SEQ ID NO 2326; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigen
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovarian and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 169 AA;
 XX
 Query Match 25.4%; Score 244.5; DB 23; Length 169;
 Best Local Similarity 38.1%; Pred. No. 9,5e-18;
 Matches 48; Conservative 34; Mismatches 39; Indels 5; Gaps 2;
 QY 64 LKANPKERICRVFSTSPAKDSLSEDFDLVSFSDTTPDIKSHYAFRFPDDGTL 123
 Db 47 LQENPKERIVAFS-EDGSGNTLFDVDMFVLCESAPRELKANYAFIYDPTDNFI 105
 QY 124 NRDLRLVNCITGEEEDTRLASSEKOLIDNLEESDIDRGTINLSEFQHYISRPD 183
 Db 106 CKEDLELTARLT----KSELDEEYVLCVKYIEADVDGDKLGFADPMIAKAPDF 161
 QY 184 ASSEFK 169
 Db 162 LSTFHI 167
 RESULT 15
 ID AAY11976 standard; protein; 120 AA.
 XX
 AC AAY11976;
 XX
 DT 18-JUN-1999 (first entry)
 XX
 DE Human 5' EST secreted protein SEQ ID NO: 576.
 XX
 KY Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KM forensic; gene therapy; chromosome mapping; signal peptide; prostate;
 KW upstream regulatory sequence; cytokine activity; cell proliferation;
 KM differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KM thrombolytic; anti-inflammatory; tumour inhibition.
 XX
 OS Homo sapiens.
 XX
 PN WO9906550-A2.
 XX
 PD 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98WO-IB01232.
 XX
 PR 01-AUG-1997; 97US-0905144.
 XX
 PA (GEST) GENSET.
 XX
 PI Duclert A, Dumas Milne Edwards J, Lacroix B;
 XX
 DR WPI: 1999-153780/13.
 XX
 DR N-PSDB; AAX40698.
 XX
 PT New isolated prostate-derived nucleic acids - used to develop
 PT products which may have cytokine, immune regulatory, haematopoiesis
 PT regulating, anti-inflammatory or tumour inhibition activity
 XX
 PS Claim 34; Page 664; 675pp; English.

CC AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins expressed in prostate, and encode the proteins
 CC given in AAX11716 to AAX11932 respectively. The proteins given represent
 CC the signal peptide and an N-terminal fragment of a secreted protein. The
 CC nucleic acid sequences can be used for producing secreted human gene
 CC products. They can also be used to develop products for diagnosis and
 CC therapy. The proteins obtained may have cytokine activity, cell
 CC proliferation and differentiation activity, haematopoiesis, regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptides can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell.

XX
 SQ Sequence 120 AA;

Query Match 22.98; Score 220; DB 20; Length 120;
 Best Local Similarity 66.28; Pred. No. 2.3e-15;
 Matches 45; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 MGSGSRSLSKELAEYODLFTFKOETLLAHRRCCELLPOQRVSSSLAQVPEQILS 60
 Db 1 MGSGSRSLSKELAEYODLFTFKOETLLAHRRCCELLPOQRXSRHFGHKCPSRFA 60
 QY 61 LPEIKANP 68
 Db 61 FOSSRPTP 68

Search completed: November 21, 2002, 17:59:33
 Job time : 36 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 21, 2002, 17:57:51 ; Search time 12 Seconds

(without alignments)
660.165 Million cell updates/sec

Title: US-09-878-454a-2

Perfect score: 962
Sequence: 1 MGSGSRLSKELAEYODLT.....EFQHVISRPDPASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	962	100.0	191	1	KIP1_HUMAN
2	909	94.5	191	1	KIP1_MOUSE
3	908	94.4	191	1	KIP1_RAT
4	345	35.9	187	1	KIP2_MOUSE
5	343	35.7	187	1	KIP2_HUMAN
6	216.5	22.5	177	1	CALB_NAERG
7	210.5	21.9	174	1	CALB_SCHPO
8	199.5	20.7	174	1	CALB_NECRC
9	199.5	20.7	174	1	CALB_YEAST
10	186.5	19.4	169	1	CALB_HUMAN
11	186.5	19.4	169	1	CALB_MOUSE
12	178.5	18.6	170	1	CALC_DROME
13	178	18.5	170	1	CA22_MOUSE
14	174.5	18.1	170	1	CALB_DROME
15	173	18.0	174	1	CA22_HUMAN
16	172.5	17.9	178	1	CALC_MOUSE
17	171.5	17.8	186	1	FREO_DROME
18	170.5	17.7	175	1	CALC_RAT
19	166.5	17.3	189	1	NCS2_CAEEL
20	158	16.4	190	1	NCS2_CAEEL
21	152.5	15.9	195	1	APLC_APLCA
22	151	15.7	189	1	H520_HUMAN
23	151	15.7	189	1	NCS1_HUMAN
24	146	15.2	190	1	NCS1_XENLA
25	146	15.2	192	1	VIS1_CAEEL
26	146	15.2	192	1	VIS1_CHICK
27	145	15.1	192	1	VIS3_MOUSE
28	140	14.6	189	1	NCAH_DROME
29	137	14.2	190	1	VIS7_RAT
30	136.5	14.2	214	1	TESC_HUMAN
31	136	14.1	192	1	NCAD_MOUSE
32	135	14.0	192	1	HIPP_HUMAN
33	131	13.6	192	1	NCAD_CHICK

34	130.5	13.6	172	1	CATR_MOUSE
35	130.5	13.6	214	1	TESC_MOUSE
36	130	13.5	192	1	NCAD_HUMAN
37	130	13.5	192	1	NECX_APLCA
38	130	13.5	791	1	KDGB_HUMAN
39	129	13.4	189	1	NCS1_SCHPO
40	128	13.3	190	1	VIS1_HUMAN
41	128	13.3	804	1	KDGB_HUMAN
42	127.5	13.3	172	1	CAT2_HUMAN
43	126.5	13.1	195	1	H520_MOUSE
44	124.5	12.9	801	1	KDGB_RAT
45	124	12.9	189	1	NCS1_YEAST

ALIGNMENTS

RESULT 1
ID KIP1_HUMAN STANDARD: PRT; 191 AA.
AC Q99828; 000735; 000693; Q99971; Q96J54;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and Integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE Interacting protein 1 (kinase interacting protein) (KIP) (CIB) (SNK
DE Interacting protein 2-28) (SIP2-28).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins."
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=98040126; PubMed=9372844;
RT Wu X., Lieber M.R.;
RT "Interaction between DNA-dependent protein kinase and a novel protein,
RT KIP."
RT Mutat. Res. 385:13-20(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=97184102; PubMed=9030514;
RT Naik U.P., Patel P.M., Parise L.V.;
RT "Identification of a novel calcium-binding protein that interacts
RT with the Integrin alphaIIb cytoplasmic domain."
RT J. Biol. Chem. 272:4651-4654(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284952; PubMed=10826701;
RT Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RT "Genomic structure of mouse and human genes for DNA-PKcs interacting
RT protein (KIP)."
RT DNA Seq. 10:415-418(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP STRUCTURE BY NMR OF 9-191.
RX MEDLINE=20283154; PubMed=10822252;
RT Huang P.M., Vogel H.J.;
RT "Structures of the platelet calcium- and integrin-binding protein and
RT the alphaIIb-integrin cytoplasmic domain suggest a mechanism for
RT calcium-regulated recognition: homology modelling and NMR studies."
RT J. Mol. Recognit. 13:83-92(2000).
CC -!- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-

CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN.
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK.
 CC -1- TISSUE SPECIFICITY: UBQUITOUS.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U83236; AAB39758.1; -
 CC EMBL: U85611; AAB53387.1; -
 CC EMBL: U82226; AAC51106.1; -
 CC EMBL: AB021866; BAA36281.1; -
 CC EMBL: BC000846; AAH00846.1; -
 CC PDB: 1DGV; 08-DEC-99.
 CC Gene: HGNC:16920; CIB1.
 CC MIM: 602293; -
 CC InterPro: IPR002048; EF-hand.
 CC Pfam: PF00036; ehand; 2.
 CC Prodom: PD000012; EF-hand; 1.
 CC SMART: SM00054; Eph; 2.
 CC PROSITE: PS00018; EF-hand; 2.
 CC Calcium-binding; Repeat; 3d-structure.
 CC CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 CC FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
 CC FT CONFICT 44 44 T -> S (IN REF. 3 AND 5).
 CC SO SEQUENCE 191 AA; 21717 MW; 9A6EA7897881E55 CRC64;
 CC
 CC Query Match 100.0%; Score 962; DB 1; Length 191;
 CC Best Local Similarity 100.0%; Pred. No. 4.3e-70;
 CC Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 MGSSGRLSKELAEYODLFLFKOELLAAHREFCELLPOEQTVESSRLAQVPEFOIIS 60
 CC DB 1 MGSSGRLSKELAEYODLFLFKOELLAAHREFCELLPOEQTVESSRLAQVPEFOIIS 60
 CC QY 61 LPELKNPFERKICRVFSTSPANDSLSFEDFDLISVFSPTATPDIKSHYAFRIPEDDDD 120
 CC DB 61 LPELKNPFERKICRVFSTSPANDSLSFEDFDLISVFSPTATPDIKSHYAFRIPEDDDD 120
 CC QY 121 GTLNREDLSLVNCLGEGEDTRLASSEKQKIDNILESDIDRDCTINLSEFOHVISRS 180
 CC DB 121 GTLNREDLSLVNCLGEGEDTRLASSEKQKIDNILESDIDRDCTINLSEFOHVISRS 180
 CC QY 181 PDFASSFKIVL 191
 CC DB 181 PDFASSFKIVL 191
 CC
 CC RESULT 2
 CC KIP1_MOUSE
 CC ID KIP1_MOUSE
 CC STANDARD; PRT; 191 AA.
 CC AC 0920F4;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 CC interacting protein) (Kinase interacting protein) (KIP) (CIB).
 CC GN CIB1 OR PKDCIP OR KIP OR CIB.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID-10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC DR TISSUE-Kidney;
 CC

RX MEDLINE-99069785; PubMed-9852683;
 RA Seki N., Hayashi A., Abe M., Araki R., Fujimori A., Fukumura R.,
 RA Hattori A., Kozuma S., Ohira M., Hori T., Saito T.;
 RT "Chromosomal assignment of the gene for human DNA-PKcs interacting
 RT protein (KIP) on chromosome 15q25.3-q26.1 by somatic hybrid analysis
 RT and fluorescence in situ hybridization.";
 RL J. Hum. Genet. 43:275-277(1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN-C57BL/6; TISSUE-Fetal kidney;
 RX MEDLINE-99160477; PubMed-10051332;
 RA Saito T., Seki N., Hattori A., Hayashi A., Abe M., Araki R.,
 RA Fujimori A., Fukumura R., Kozuma S., Matsuda Y.;
 RT "Structure, expression profile, and chromosomal location of a mouse
 RT gene homologous to human DNA-PKcs interacting protein (KIP) gene.";
 RL Mamm. Genome 10:315-317(1999).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP Naik M.U., Naik U.P.;
 RA "Cloning and tissue distribution of murine calcium and integrin
 RA binding protein, CIB.";
 RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN-C57BL/6J;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Bozell D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokura K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohlsuk S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- TISSUE SPECIFICITY: UBQUITOUS.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB006463; BAA74429.1; -
 CC EMBL: AB017361; BAA36165.1; -
 CC EMBL: AF173010; AAG38960.1; -
 CC EMBL: AK010345; BAB26868.1; -
 CC HSP: O99828; 1DGV.
 CC MGD: MGI:134418; CIB1.
 CC InterPro: IPR002048; EF-hand.
 CC Pfam: PF00036; ehand; 2.
 CC Prodom: PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF-HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA-BIND 116 127
 FT CA-BIND 161 172 EF-HAND 1 (POTENTIAL).
 FT CA-BIND 161 172 EF-HAND 2 (POTENTIAL).
 SO SEQUENCE 191 AA; 21763 MW; C85B603A19FD9AC CRC64;

Query Match 94.5%; Score 909; DB 1; Length 191;
 Best Local Similarity 94.2%; Pred. No. 7.2e-66;
 Matches 180; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGGSSRLSKELLAEYQDLFTLTKOELLARHRCCELLPOBORVYESSLRAPVEEQILS 60
 DB 1 MGGSSRLSKELLAEYQDLFTLTKOELLARHRCCELLPPQGRVYESSLRHVSFEQILS 60
 QY 61 LPELKANFKERICVFSTSPAKDSLFEDFLDLVSFSDTATPDIKSHYAFRIEDFDD 120
 DB 61 LPELKANFKERICVFSTSPAKDSLFEDFLDLVSFSDTATPDIKSHYAFRIEDFDD 120
 QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMKNOLINDILEESDIDRDGTINLSEFOHVSRS 180
 DB 121 GTLNREDLSRLVNCITGEGEDTRLASSEMKNOLINDILEESDIDRDGTINLSEFOHVSRS 180
 QY 181 PDFASSEKIVL 191
 DB 181 PDFASSEKIVL 191

RESULT 3

KIP1_RAT

ID KIP1_RAT STANDARD; PRT; 191 AA.

AC G99010;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs interacting protein) (Kinase interacting protein) (KIP) (CIB).

GN CIB1 OR PRKDCIP OR KIP OR CIB.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID-10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-99452760; Pubmed-10523297;

RA Kusselmann G., Weller M., Wulff P., Jessberger S., Konietzko U.,

RA Saefeldi J., Staudil U., Bereliter-Hahn J., Streibhardt K., Kuhl D.,

RT "The polo-like protein kinases Pnk and Snk associate with a Ca(2+)-and integrin-binding protein and are regulated dynamically with synaptic plasticity";

RL EMBL J. 18:5528-5539(1999).

CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN CYTOPLASMIC DOMAIN (BY SIMILARITY).

CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY SIMILARITY).

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL; AF136585; AAF0368.1; -
 DR HSSP; G99828; IDGV.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 2.
 DR ProDom; PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF-HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA-BIND 116 127
 FT CA-BIND 161 172 EF-HAND 1 (POTENTIAL).
 FT CA-BIND 161 172 EF-HAND 2 (POTENTIAL).
 SO SEQUENCE 191 AA; 21800 MW; 3B00B0228879CC7 CRC64;

Query Match 94.4%; Score 908; DB 1; Length 191;
 Best Local Similarity 94.2%; Pred. No. 8.7e-66;
 Matches 180; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGGSSRLSKELLAEYQDLFTLTKOELLARHRCCELLPOBORVYESSLRAPVEEQILS 60
 DB 1 MGGSSRLSKELLAEYQDLFTLTKOELLARHRCCELLPPHRTVYESSLRHVSFEQILS 60
 QY 61 LPELKANFKERICVFSTSPAKDSLFEDFLDLVSFSDTATPDIKSHYAFRIEDFDD 120
 DB 61 LPELKANFKERICVFSTSPAKDSLFEDFLDLVSFSDTATPDIKSHYAFRIEDFDD 120
 QY 121 GTLNREDLSRLVNCITGEGEDTRLASSEMKNOLINDILEESDIDRDGTINLSEFOHVSRS 180
 DB 121 GTLNREDLSRLVNCITGEGEDTRLASSEMKNOLINDILEESDIDRDGTINLSEFOHVSRS 180
 QY 181 PDFASSEKIVL 191
 DB 181 PDFASSEKIVL 191

RESULT 4

KIP2_MOUSE

ID KIP2_MOUSE STANDARD; PRT; 187 AA.

AC Q92309;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Kinase interacting protein 2 (KIP 2).

GN KIP2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID-10090;

RN [1]

RP SEQUENCE FROM N.A.

RX TISSUE-Brain, and Testis;

RX MEDLINE-99132027; Pubmed-9931475;

RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,

RA Saito T.;

RT "Structure, expression profile and chromosomal location of an isoform of DNA-PKcs interacting protein (KIP) gene";

RL Biochim. Biophys. Acta 1444:143-147(1999).

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL; AB016080; BAA36545.1; -
 DR HSSP; G99828; IDGV.
 DR MGD; MGI:1929293; KIP2.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF-HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA-BIND 116 127
 FT CA-BIND 157 168 EF-HAND 1 (POTENTIAL).
 FT CA-BIND 157 168 EF-HAND 2 (POTENTIAL).
 SO SEQUENCE 187 AA; 21703 MW; D21D21DCBDB65FC CRC64;

	Query Match	Similarity	35.9%	Score 345;	DB 1;	Length 187;
	Best Local	Similarity	37.8%	Pred. No. 6.6e-21;		
	Matches	73;	Conservative	43;	Mismatches	65;
					Indels	12;
					Gaps	4
QY	1	MGGSSRLSKELLAYODITFTYKOEILLAHRRFCE---	LLPQORTYESSLRACVPEE	56		
DB	1	MGNKOTITTELEOLDYQOCTFFNKKDILKLAHFFELAPNVLPMYDR---	KSPIYHVPMS	57		
QY	57	QILSLPELKANDPERICRVSTSPAKDSLEPDLILSVSDRATPIDIKHYARIPD	116			
DB	58	LIIQHPLELRPNFKRIVYEARS-EDGEKNLITNDVDVDFSVLCESAPRLKANYAKYID	116			
QY	117	FDDDLTLNRDL SRLVNCITTEGEGDYRLSASEMKOLINILTEESDIDRDTINLSFCOH	176			
DB	117	FNTDHFICKEDIEMLTARLT---KSELEDEDEVALYCDRIVEADDDGGRKIGFADFEM	172			
QY	177	ISRSPPDFASSFKI	189			
DB	173	IAKADEFLSTFHI	185			

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OY      1  MGSGGSLKSLKLLAEYODTLFLTKOEILLAHKRFCE---LLPQDRTVESSLRAQVPE 56
II      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
AC ID      KIP2_HUMAN      STANDARD;      PRT;      187 AA.
AC 075838;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kinase interacting protein 2 (KIP 2).
GN KIP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=99132027; PubMed=9931475;
RA Seki T., Hattori A., Hayashi A., Kozuma S., Ohira M., Hoti T.,
RA Saito T.,
RT "Structure, expression profile and chromosomal location of an Isolog
RT of DNA-PKcs interacting protein (KIP) gene.";
RT Blochlm. Biophys. Acta 1444:143-147(1999).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AB012955; BAA33584.1; -
CC HSSP; O99828; IDGV.
DR DR MTR; 605564; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR Prodom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00016; EF_HAND; 2.
DR Calcium-binding; Repeat.
KW CA BIND 116 127 EF-HAND 1 (POTENTIAL).
FT CA BIND 157 168 EF-HAND 2 (POTENTIAL).
FT FT 157 168 EF-HAND 2 (POTENTIAL).
SQ SEQUENCE 187 AA; 21643 MW; D51FEC234D31BEF CRC64;

Query Match 35.7%; Score 343; DB 1; Length 187;
Best local Similarity 37.8%; Pred. No. 9.6e-21;
Matches 73; Conservative 43; Mismatches 65; Indels 12; Gaps 4;

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[illegible]

RESULT 6	STANDARD:	PRT:	177 AA.
AC CALB_NAEGR			
AC P42322;			
DT 01-NOV-1995 (Rel. 32, Created)			
DT 01-NOV-1995 (Rel. 32, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)			
DE (calcineurin regulatory subunit).			
GN CNB1.			
OS Neogleria gruberl.			
CC Eukaryota: Heterolobossea; Schizopyrenida; Vahlkampfiidae; Neogleria.			
OX NCBI_TaxID=5762;			
LN [1]			
RN SEQUENCE FROM N.A.			
RP STRAIN-NEG;			
RC MEDLINE=95172399; PubMed=7867946;			
RA Remillard S.P., Lai E.Y., Levy Y.Y., Fulton C.;			
RT "A calcineurin-B-encoding gene expressed during differentiation of			
RT the amoeboid flagellate Neogleria gruberi contains two introns."			
RL Gene 154:39-45(1993).			
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN. A CALCIUM-DEPENDENT,			
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM			
CC SENSITIVITY (BY SIMILARITY).			
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY			
CC SUBUNIT (B) (BY SIMILARITY).			
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING			
CC SITES (BY SIMILARITY).			
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.			
CC -----			
CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/sib.ch).			
CC or send an email to license@sib-sib.ch .			
CC -----			
DR EMBL: U04380; AAA81896.1; -			
DR HSSP: P06705; IAU1.			
DR InterPro: IPR002048; EF-hand.			
DR Pfam: PF00036; EF-hand; 4.			
DR ProDom: PD000012; EF-hand; 2.			
DR SMART: SM00054; Efn; 4.			
DR PROSITE: PS00018; EF_HAND; 4.			
CC Calcium-binding: Repeat.			
FT CA_BIND 38 49 EF-HAND 1 (BY SIMILARITY).			
FT FT 70 81 EF-HAND 2 (BY SIMILARITY).			
FT CA_BIND 107 118 EF-HAND 3 (BY SIMILARITY).			
FT CA_BIND 148 159 EF-HAND 4 (BY SIMILARITY).			
SO SEQUENCE 177 AA; 20057 MW; 01D448E6947E97C CRC64;			
Query Match 22.5%; Score 216.5; DB 1; Length 177;			
Best Local Similarity 29.2%; Pred. NO. 1.1e-10;			
Matches 52; Conservative 40; Mismatches 73; Indels 13; Gaps 3;			

Db 1 MGNTSSLRPEVEEMKGTNFTOKKIKYKREKIDKNGTISK-----DEFLM 52

QY 61 LPELKANPEKRICRVFSTSPAKDSLSFEDFDLDSVSDTATPDIKSHAFRIEDDD 120

Db 53 IPELVANPELVKRVISFDEN-GDGSVNFKEFIATLSTFNQSGKRLERAFYVIDD 111

QY 121 GTLNREDLSRLVNCGLTGEEDTSLASSEMKQIDNILEESDIDRGTINLSEFOHVS 178

Db 112 GTISNELFTVLKMGV---NMLSDVOLQOIVDKTILEADEDDGDKISFEERAKTLS 165

RESULT 7

CaLB_SCHPO STANDARD: PRT: 174 AA.

AC Q9093; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)

DE (Calcineurin regulatory subunit).

GN CNB1 OR SPCC830.06.

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OX Schizosaccharomycetes.

NCBI_TaxID=4896;

SEQUENCE FROM N.A.

STRAIN=972.

Medline=21848401; PubMed=11859360;

Wood V., Swilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Voiclaert G., Aert R., Robben J., Grymoprez B., Weltens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritze C., Holzer E., Moesli D., Hilbert H., Eger P., Zimmermann W., Medler H., Mambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Lucas M., Kochet M., Galliard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Sipakovskii G.V., Ussery D., Barrett B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe." Nature 415:871-880(2002).

CaLMODULIN REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM SENSITIVITY (BY SIMILARITY).

-1- SUBUNIT COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY SUBUNIT (B) (BY SIMILARITY).

-1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES (BY SIMILARITY).

-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL: AL109850; CAB52879.1; -

DR HSSP: P06705; 1A01.

DR InterPro: IPR002048; EF-hand.

DR InterPro: IPR001125; Recoverin.

DR Pfam: PF00036; efhand; 4.

DR PRINTS: PR00450; RECOVERIN.

DR Prodom: PD000012; EF-hand; 1.

DR SMART: SM00054; EFh; 4.

DR PROSITE: PS00018; EF_HAND; 4.

KW Calcium-binding; Myristate.

FT CA_BIND 34 45 EF-HAND 1 (BY SIMILARITY).

FT CA_BIND 66 77 EF-HAND 2 (BY SIMILARITY).

FT CA_BIND 103 114 EF-HAND 3 (BY SIMILARITY).

FT CA_BIND 144 155 EF-HAND 4 (BY SIMILARITY).

SO SEQUENCE 174 AA; 19675 MW; EEF38FE74959442E CRC64;

Query Match 21.9%; Score 210.5; DB 1; Length 174;

Best Local Similarity 27.2%; Pred. No. 3; 2e-10;

Matches 49; Conservative 46; Mismatches 68; Indels 17; Gaps 4;

QY 1 MGSGSRLSKELIAEYODLFTLRKOBILAHRRFCELLPQEQRTVSSSLRAQVPEQILS 60

Db 1 MGOSQSFIEDLISN-----SFSNEIETIRKRFIR-----IDANSGSIDRNEFLS 48

QY 61 LPELKANPEKRICRVFSTSPAKDSLSFEDFDLDSVSDTATPDIKSHAFRIEDDD 120

Db 49 IPSVANPPLASRLFSVDEDDGGD-VDPOEFINSLSFVHGKKEKLFARITYIDND 107

QY 121 GTLNREDLSRLVNCGLTGEEDTSLASSEMKQIDNILEESDIDRGTINLSEFOHVS 180

Db 108 GTISNELFTVLKMGV---NMLSDVOLQOIVDKTILEADEDDGDKISFEERKDIVSS 163

RESULT 8

CaLB_NEUCR STANDARD: PRT: 174 AA.

AC P87072; 013408; 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)

DE (Calcineurin regulatory subunit).

GN CNB-1 OR CAN-B.

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;

SEQUENCE FROM N.A.

STRAIN=74A;

Medline=98007857; PubMed=9349701;

RX Prokisch H., Yarden O., Dieminger M., Tropeck M., Barthelmeß I.B.; "Impairment of calcineurin function in Neurospora crassa reveals its essential role in hyphal growth, morphology and maintenance of the apical Ca2+ gradient." Mol. Gen. Genet. 256:104-114(1997).

CaLMODULIN REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM SENSITIVITY.

-1- SUBUNIT COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY SUBUNIT (B).

-1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES.

-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

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DB 1 GAAPSKIVDLEED-----INFDEIERLRKREMKLRDSSGSDKN-----EFMSI 48
 QY 62 PELKANPEKRICRVSTSPAKDSLFEDFLDLSTFSPATPDISHAFREDDDG 121
 DB 49 PGVSSNPLAGRIEVEFDADNSD-VDFEFTGLSTFSGSGSDEKIRAFKIIDDKG 107
 QY 122 TNRDLSLVNCLTGEEDFTLSASEMQLIDNILEESDIDRDGTINSEPOHY 177
 DB 108 FLSNGBLFIYKIMG-----SNLDBDQLQIYDRIIVENDSGDGNLSFEERNAL 159

RESULT 10
 CALB_HUMAN
 ID CALB_HUMAN STANDARD: PRT: 169 AA.
 AC P06705; P15117; 008044:
 DT 01-JAN-1988 (Rel. 06, Create#)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform 1).
 GN PPP3R1 OR CNB OR CNA2.
 OS Homo sapiens (Human).
 OS Bos taurus (Bovine).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_Taxid=9606, 9913, 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human;
 RX MEDLINE=90126237; PubMed=2558868;
 RA Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
 RT "Isolation and sequence of a cDNA clone for human calcineurin B, the Ca²⁺-binding subunit of the Ca²⁺/calmodulin-stimulated protein phosphatase.";
 RL DNA 8:675-682(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Bovine;
 RA Margang C.E., Bottorff D.A., Adachi K.;
 RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-168.
 RC SPECIES-Bovine; TISSUE-Brain;
 RX MEDLINE=84132092; PubMed=6321184;
 RA Altken A., Klee C.B., Cohen P.;
 RT "The structure of the B subunit of calcineurin.";
 RL Eur. J. Biochem. 139:663-671(1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Rat;
 RA Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC SPECIES-Rat; TISSUE-Brain, and Testis;
 RX MEDLINE=94153993; PubMed=8110831;
 RA Chang C.-D., Mukai H., Kuno T., Tanaka C.;
 RT "cDNA cloning of an alternatively spliced isoform of the regulatory subunit of Ca²⁺/calmodulin-dependent protein phosphatase (calcineurin B alpha 2).";
 RL Biochim. Biophys. Acta 1217:174-180(1994).
 RN [6]
 RP CALCIUM-BINDING DATA.
 RC SPECIES-Bovine;
 RX MEDLINE=80101597; PubMed=293720;
 RA Klee C.B., Crouch T.H., Krinks M.H.;
 RT "Calcineurin: a calcium- and calmodulin-binding protein of the nervous system.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

RC SPECIES-Bovine;
 RX MEDLINE=95360994; PubMed=7543369;
 RA Griffith J.P., Kim J.L., Kim E., Shtechak M.D., Thomson J.A.,
 RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Nevia M.A.;
 RT "X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant FKBP12-FK506 complex.";
 RL Cell 82:507-522(1995).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RC SPECIES-Human;
 RX MEDLINE=9609707; PubMed=8524402;
 RA Kissinger C.R., Farge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,
 RA Tempczyk A., Kalish V.J., Tucker R.D., Showalter R.E., Moosaw E.W.,
 RA Gastline L.N., Habuka N., Chen X., Maldonado F., Barker J.E.;
 RA Baquet R., Villafraña J.E.;
 RT "Crystal structures of human calcineurin and the human FKBP12-FK506-calcineurin complex.";
 RL Nature 378:641-644(1995).
 CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM SENSITIVITY.
 CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY SUBUNIT (B).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING IN RAT.
 CC -1- TISSUE SPECIFICITY: ISOFORM 2 IS TESTIS-SPECIFIC.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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 DR EMBL; M30773; AAB08721.1; -
 DR EMBL; X71666; CA50659.1; -
 DR EMBL; L03554; AAA40854.1; -
 DR EMBL; D14568; BAA03422.1; -
 DR EMBL; D14425; BAA03318.1; -
 DR PIR; A33391; A33391.
 DR PIR; S34127; S34127.
 DR PIR; J70297; J70297.
 DR PIR; S42716; S42716.
 DR PIR; S42717; S42717.
 DR PDB; 1AUI; 03-FEB-97.
 DR PDB; 1TCO; 12-FEB-97.
 DR GeneW; HGNC:9317; PPP3R1.
 DR MIM; 601302; -
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 4.
 DR PRODOM; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 KW Calcium-binding; Repeat; Alternative splicing; Myristate;
 KM 3D-structure.
 FT INIT_MET 0
 FT LIPID 1
 FT CA_BIND 30
 FT CA_BIND 62
 FT CA_BIND 99
 FT CA_BIND 140
 FT CA_BIND 151
 FT VARSPLIC 1
 FT MYRSTATE 1
 FT EF_HAND 1
 FT EF_HAND 2
 FT EF_HAND 3
 FT EF_HAND 4
 FT G->MEQTDLOSQIFPEKNEKNGKXKHFRONKYPFSR
 FT ELVNLIPADKRG (IN ISOFORM 2).
 FT C->S (IN REF. 3).
 FT C->S (IN REF. 3).
 FT SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;
 Query Match 19.4%; Score 186.5; DB 1; Length 169;
 Best Local Similarity 31.1%; Pred. No. 2.5e-08;

Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

QY 56 EQILSLPELKANFKERICRVSTSPAKDLSLSEDFDLISVSDTATPDIKSHYARIF 115
 DB 40 EEFMSLPELQANPLVGRVIDIFDTD-GNGEVDKEFEFEGVSQSVKGDQKRFARIRY 98

QY 116 DFDDDGTLNREDLSRLVNCVTGEGEDTRLASASEMKOLINDLEESDIDRGDTINLSEFOH 175
 DB 99 DMDKDGYSNGELFQVLKMMVGVG---NNLKDTQLQIIVDTIINADKDGGRISFEFCA 154

QY 176 VI 177
 DB 155 VV 156

RESULT 11
 CALB_MOUSE STANDARD; PRT; 169 AA.

ID CALB_MOUSE STANDARD; PRT; 169 AA.

AC 063810;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1)
 DE Calcineurin B subunit isoform 3 regulatory subunit B alpha isoform 1)
 GN PPP3R1 OR CNB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=9239379; PubMed=1325794;
 RA Ueki K., Muramatsu T., Kincaid R.L.;
 RT "Structure and expression of two isoforms of the murine calcmodulin-dependent protein phosphatase regulatory subunit (calcineurin B).";
 RL Biochem. Biophys. Res. Commun. 187:537-543(1992).
 CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONERS CALCIUM SENSITIVITY.
 CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY SUBUNIT (B).
 CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC EMBL; S43864; AAB23171.1;
 DR HSSP; P06705; IATU
 DR MGD; MGI:107172; Ppp3r1.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 4.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 KM Calcium-binding; Repeat; Myristate.
 FT INIT_MER 0
 FT LIPID 1
 FT CA_BIND 30 41 MYRISTATE (BY SIMILARITY).
 FT CA_BIND 62 73 EF-HAND 1.
 FT CA_BIND 99 110 EF-HAND 2.
 FT CA_BIND 140 151 EF-HAND 3.
 FT CA_BIND 169 AA; 19142 MW; D1490BA5BD2F432F CRC64;
 SEQUENCE

Query Match 19.4%; Score 186.5; DB 1; Length 169;
 Best Local Similarity 31.1%; Pred. No. 2.5e-08;
 Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

QY 56 EQILSLPELKANFKERICRVSTSPAKDLSLSEDFDLISVSDTATPDIKSHYARIF 115
 DB 40 EEFMSLPELQANPLVGRVIDIFDTD-GNGEVDKEFEFEGVSQSVKGDQKRFARIRY 98

QY 116 DFDDDGTLNREDLSRLVNCVTGEGEDTRLASASEMKOLINDLEESDIDRGDTINLSEFOH 175
 DB 99 DMDKDGYSNGELFQVLKMMVGVG---NNLKDTQLQIIVDTIINADKDGGRISFEFCA 154

QY 176 VI 177
 DB 155 VV 156

RESULT 12
 CALC_DROME STANDARD; PRT; 170 AA.

ID CALC_DROME STANDARD; PRT; 170 AA.

AC 024214; Q9V315;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcineurin B subunit, isoform 2 (Protein phosphatase 2B regulatory subunit).
 DE CANB2 OR CNB2 OR CG11217.
 GN Drosophila melanogaster (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cancon-S;
 RX MEDLINE=97080515; PubMed=8921860;
 RA Warren W.D., Phillips A.M., Howells A.J.;
 RT "Drosophila melanogaster contains both X-linked and autosomal homologs of the gene encoding calcineurin B.";
 RL Gene 177:149-153(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Abmayr A., An H.-J., Andrews-Frankoch C., Baldwin D., Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borrova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P., Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K., Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C., Jaitli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Klup D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mated B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson Z.M., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT The genome sequence of *Drosophila melanogaster*.
RL Science 287:2185-2195(2000)
CC -1- FUNCTION: CALNEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS. IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U56245; AAC47350.1; -
DR EMBL: AE003840; AAF59195.1; ALT_SEQ.
DR HSSP: P06705; ITCO.
DR Flybase: FBgn0015614; Canb2.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001125; Recoverin.
DR Pfam: PF00036; ehand; 4.
DR PRINTS: PR00450; RECOVERIN.
DR PRODOM: PD000012; EF-hand; 2.
DR SMART: SM00054; Eph; 4.
DR PROSITE: PS00018; EF_HAND; 4.
DR KMW Calcium-binding; Repeat.
DR FT CA_BIND 31 42 EF_HAND 1 (POTENTIAL).
DR FT CA_BIND 63 74 EF_HAND 2 (POTENTIAL).
DR FT CA_BIND 100 111 EF_HAND 3 (POTENTIAL).
DR FT CA_BIND 141 152 EF_HAND 4 (POTENTIAL).
DR CA_BIND SEQUENCE 170 AA; 19267 MW; FDB1BD9DB5A4BDEC CRC64;
SQ
Query Match 18.6%; Score 178.5; DB 1; Length 170;
Best Local Similarity 24.7%; Pred. No. 1,1e-07;
Matches 44; Conservative 43; Mismatches 72; Indels 19; Gaps 4;
OY 3 GGGSRKSKELLAEYDGLFLTNQELLARPCCELLPQORVVESSLRAQVFEEQLSLP 62
DB 2 GNETSLPMEKCSNFD-----ADEIRRLGKRP-----RTLDNSGALSVDKMSLP 47
OY 63 EKAKPFRERIGRVSTSPAKSLSFEDFLDLSTVSDATPDTSHTVFRFPDDGCT 122
DB 48 ELQGNPLVQVRYDITFD-ADGNGEVPFKETQGVSGKDKLSLRLEFRIDYMDNDXY 106
OY 123 LNRDLASRLVNCITGEGEDTRLSASEKQLDNIIEESPIDRGTINSEPHYISRS 180
DB 107 ISNGELFQVLKMMVG-----NNLKDTQLOQIYDKITGFADKDEGKISFDEFCVVGNT 160

DE homologous protein) (S1d470).
GN CHP.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
CC Eumariota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE-Liver;
RX MEDLINE=96215311; PubMed=6626580.
RA Barros M.R., Bernd K.K., Devitt N.D., Chang A., Mills K.,
RA Szul E.S.,
RT "A novel Ca2+-binding protein, p22, is required for constitutive
RT membrane traffic."
RL J. Biol. Chem. 271:10183-10187(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE-Brain;
RX MEDLINE=21374135; PubMed=11481038;
RA Matsumoto M., Miyake Y., Nagita M., Inoue H., Shitakubo D.,
RA Takemoto K., Ohtsuka C., Murakami H., Nakamura N., Kanazawa H.,
RT "A serine/threonine kinase which causes apoptosis-like cell death
RT interacts with a calneurin B-like protein capable of binding Na+/H+
RT exchanger."
RL J. Biochem. 130:217-225(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.,
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse; STRAIN=C57BL/6J; TISSUE-Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Hara A., Fukunishi Y., Konno H., Aoechi J., Fukuda S.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gasterland T., Gissi C., Kling B., Kochwa H.,
RA Kuenl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schmitt L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hornum M., Humm D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: UNIDIRECTIONALLY EXPRESSED.
CC -1- PFM: BOTH N-XYRISTOTYLATION AND CALCIUM-MEDIATED CONFORMATIONAL
CC CHANGES ARE ESSENTIAL FOR ITS FUNCTION.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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CC -----
DR EMBL: U39875; AB04146.1; -
DR EMBL: AB070350; BAB5369.1; -
DR EMBL: AB025217; BAA84688.1; -

DR EMBL: AK005067; BAB23791.1; -
 DR HSSP: P06705; 1AUI.
 DR MGD: MGI:1927185; Chp.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ethand; 3.
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 2.
 DR PROSITE: PS00018; EF-HAND; 1.
 DR Calcium-binding; Repeat; Myristate.
 FT INIT-MET 0
 FT LIPID 1
 FT DOMAIN 38 49 MYRISTATE (PROBABLE).
 FT CA-BIND 70 81 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
 FT CA-BIND 122 133 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
 FT CA-BIND 166 174 EF-HAND 3 (BY SIMILARITY).
 FT MOTAGEN 133 133 EF-HAND 4 (BY SIMILARITY).
 FT SEQUENCE 194 AA; 22301 MW; E2DF3E5F627B8231 CRC64;
 Query Match 18.5%; Score 178; DB 1; Length 194;
 Best Local Similarity 26.8%; Pred. No. 1.4e-07;
 Matches 52; Conservative 35; Mismatches 75; Indels 32; Gaps 6;
 QY 5 GSR-----LSKELLAEFQDTFTLKQELLAAHRCPCCLLPQEQRTVSSLAQVPEQILS 60
 DB 1 GSRASSTLRDELEELKEIKETGFSGHSQITRLYSRFTSIDKNGCTLSR-----EDFOR 52
 QY 61 LPELKNPFERICRVSTSPAKDSLEFEDLLSYF-----SDATPD----- 105
 DB 53 IPELAINPLCDRIINAF-FSEGEDVNFQGFMTLAFRIEDNEKSKVDNGEPLNRS 111
 QY 106 IKSHYAFRIEDPDGDTLNEDELSTLVNCTGEGEDTRLASASEKQIDINILESDIDR 165
 DB 112 NKLFHAFRLDLDKDKISDELQVLRMVG-----VNISDEQLGSIADNTIQEADQGD 167
 QY 166 GTINLSEFOHVISR 179
 DB 168 SAISFEFEVYLER 181
 RESULT 14
 CALB_DROME STANDARD; PRT; 170 AA.
 AC P48451; Q9M4D0;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory subunit).
 GN CANB OR CNB1 OR CNB OR CNB OR CG4209.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RX MEDLINE-93054551; PubMed-1331060;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananthakrishnan P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Arlt J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Delcher A., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ileguam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
 CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS. IT IS A CALCIUM
 CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B). THE A COMPONENT IS
 CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
 CC SENSITIVITY (BY SIMILARITY).
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
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 DR EMBL: M97215; AAA28411.1; -
 DR EMBL: AE003434; AAF46026.1; -
 DR HSSP: P06705; 1TCC.
 DR FlyBase: FBgn0010014; Canb.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ethand; 4.
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 4.
 DR PROSITE: PS00018; EF-HAND; 4.
 DR Calcium-binding; Repeat.
 KW CA-BIND 31 42 EF-HAND 1 (POTENTIAL).
 FT CA-BIND 63 74 EF-HAND 2 (POTENTIAL).
 FT CA-BIND 100 111 EF-HAND 3 (POTENTIAL).
 FT CA-BIND 141 152 EF-HAND 4 (POTENTIAL).
 FT SEQUENCE 170 AA; 19341 MW; 77DB8B8BBD961900 CRC64;
 Query Match 18.1%; Score 174.5; DB 1; Length 170;
 Best Local Similarity 26.5%; Pred. No. 2.3e-07;
 Matches 41; Conservative 38; Mismatches 63; Indels 13; Gaps 3;
 QY 26 ELLAHRFCCLLPQEQRTVSSLAQVPEQILSLELKNPFERICRVSTSPAKDS 85
 DB 19 EIRRLGRF-----RKLDLNSGALSIDEFMSLELQONPLVORVIDIFD-ADNGE 69

QY 86 LSFEDFLDLVSFSDTAPDKSHVAFRIFFDDGTLNRDLRLVNCLTGEGEDTRL 145
 DB 70 YDFKEPIGVQSVFSGDKLSKLRFAFRFYDNDNGISNGELFVYLRKAVG----NNLK 125
 QY 146 ASEMQLDNIIEESDIDRDGTINLSERQHVISR 180
 DB 126 DTQLQOIVDKTICFADKDEKISFDEFCSVYGMT 160

RESULT 15
 CA22_HUMAN STANDARD: PRT; 194 AA.
 AC Q99653;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin homologous protein) (Calcineurin B homolog)
 GN CHP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RX MEDLINE-97057295; PubMed-8901634;
 RA Lin X, Barber D.L.;
 RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H exchange."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Muscle;
 RA Strausberg R.;
 CC Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE. SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: UBICUOUSLY EXPRESSED. HAS BEEN FOUND IN FETAL EYE, LUNG, LIVER, MUSCLE, HEART, KIDNEY, THYROID AND SPLEEN.
 CC -1- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 DR EMBL; U61538; AA837770.1; -
 DR EMBL; BC001646; AA01646.1; -
 DR HSSP; P06705; LAUI.
 DR MIM: 606988; -
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; efhand; 3.
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART; SM00054; Efh; 2.
 DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
 KW Calcium-binding; Repeat; Myristate; Phosphorylation.
 FT INIT_MER 0
 FT LIPID 0
 FT DOMAIN 1 1
 FT 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).

FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
 FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
 SQ SEQUENCE 194 AA; 22325 MW; 17DDEEF03C88380 CRC64;
 Query Match 18.0%; Score 173; DB 1; Length 194;
 Best Local Similarity 26.3%; Pred. No. 3.6e-07;
 Matches 51; Conservative 35; Mismatches 76; Indels 32; Gaps 6;
 QY 5 GSR-----LSKELLAEYODLTFLKQELLAHRRFCCLLQEQNTVSSSLRAQVPEQIIS 60
 DB 1 GSRASTLRLDDELEETKKTGFSHSQITRLYSRFTSLDNGETLSR-----EDFOR 52
 QY 61 LPELANPEKRIKRYFSTSPAKDSIFEDFLDLVSF-----SPTAPD----- 105
 DB 53 IPELANPFGRIINAFEE-GEQVNFEGFRTLAHFRIDENSKVNGPEPLNSNS 111
 QY 106 IKSHAFAFIFFDDGTLNRDLRLVNCLTGEGEDTRLASASEMQLDNIIEESDIDRD 165
 DB 112 NKLHFAFRLYDLKDEKISRDELQVLRLMVG-----VNISDQLGSIAQRTIQEQADQDD 167
 QY 166 GTINLSERQHVISR 179
 DB 168 SAISFTFEVYVLEK 181

Search completed: November 21, 2002, 17:58:12
 Job time : 12 secs

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OM protein - protein search, using sw model

Run on: November 21, 2002, 17:57:51 : Search time 17 Seconds

(without alignments)
1080.099 Million cell updates/sec

Title: US-09-878-454a-2

Perfect score: 962

Sequence: 1 MGSGSRLSKELAEYQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413	42.9	311	2 T21563	hypothetical prote
2	210.5	21.9	174	2 T41632	probable calcineur
3	204.5	21.3	175	2 JH0462	phosphoprotein pho
4	199.5	20.7	174	2 T47245	calcineurin regula
5	186.5	19.4	170	1 A33391	calcineurin regula
6	186.5	19.4	170	1 S34127	calcineurin regula
7	186.5	19.4	170	1 JCI320	calcineurin regula
8	186.5	19.4	216	1 S42716	calcineurin regula
9	183.5	19.1	369	2 T22708	hypothetical prote
10	178.5	18.6	170	2 JCI321	calcineurin regula
11	175.5	18.2	170	2 JCI321	calcineurin regula
12	174.5	18.1	170	2 JCI321	calcineurin regula
13	172.5	17.9	179	2 JCI321	calcineurin regula
14	170.5	17.7	165	2 PS0261	calcineurin regula
15	170.5	17.7	165	2 PS0261	calcineurin regula
16	170.5	17.7	195	2 T28047	calcineurin regula
17	170.5	17.7	213	2 T31775	hypothetical prote
18	166.5	17.3	190	2 T20725	hypothetical prote
19	164.5	17.1	226	2 T51357	hypothetical prote
20	156	16.2	190	2 T51357	calcineurin B-like
21	152.5	15.9	226	2 T08923	calcineurin B-like
22	151.5	15.7	213	2 T51356	calcineurin B-like
23	151	15.7	193	2 JH0816	calcineurin B-like
24	151	15.7	193	2 T50676	neural vistin-1lk
25	151	15.7	246	2 T05308	gene Rem-1 protei
26	151	15.7	246	2 H85387	hypothetical prote
27	150	15.6	193	2 S47565	calcium-binding pr
28	148	15.4	192	2 T01375	calcium sensor hom
29	145	15.1	190	2 A55666	neurocalcin - fru1

30	142	14.8	191	2 JH0815	neural vistin-1lk
31	141	14.7	270	2 JC7631	K+ channel-interac
32	138.5	14.4	254	2 T29566	hypothetical prote
33	138	14.3	193	2 JC2186	hippocalcin - huma
34	137	14.2	224	2 F96668	protein FIM19.5 (1
35	135	14.0	193	2 JH0616	neurocalcin (clone
36	135	14.0	195	2 JC1347	hippocalcin - rat
37	134	13.9	190	2 S58303	related to neurona
38	133	13.8	191	2 JH0605	neural vistin-1lk
39	133	13.6	172	2 S38531	vistin-1lk prote
40	130.5	13.5	791	2 A53691	caltractin - mouse
41	130	13.5	190	2 S61168	diacylglycerol kin
42	129	13.4	190	2 S61168	hypothetical prote
43	127.5	13.3	202	2 I38424	centrin - human
44	126.5	13.1	202	2 S21155	recovery - mouse
45	126	13.1	151	2 A71409	calmodulin 8 (limp

ALIGNMENTS

RESULT 1

T21563

hypothetical protein F30A10.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T21563

R/Barlow, K.
submitted to the EMBL Data Library, October 1996

A/Reference number: Z19442

A/Accession: T21563

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-311 <WILL>

A/Cross-references: EMBL:Z81072; PDB:CA03019.1; GSPDB:GND0019; CESP:F30A10.1

A/Experimental source: clone F30A10

A/Genetics:

A/Map position: 1

A/Introns: 106/2; 139/3; 190/3; 240/1

Query Match
Best Local Similarity 42.9% Score 413; DB 2; Length 311;
Matches 88; Conservative 41; Mismatches 52; Indels 26; Gaps 5;

OY	1	MGSGSRLS-----KEILAEYQDLTFLKQILLAHRRFCCLPQEQRTVSS 48
DB	111	MGNNASSLSELNLSKGVFTREQLDEYDCTFFRKDIIRLYKRYALNPKR--VPTN 167
OY	49	LRAQVP-----FQILSLPELKNPFKEKICRVSTSPAKDSLFEFDLILSVSPDA 102
DB	168	MGNRPATTLTLFEVEKMPKELKPRKICVFS-EDGKNSLFDPLDMFVSFSEA 226
OY	103	TPDKSHAFRIIPDDGTLNRDLSRLVNCLEGGEDTRLSASEMKQIDNILESDI 162
DB	227	PLOKLYAFRIYDGDGLGHDLGKMSIRLFRD---ELSDVEVEFIETRIEEDL 282
OY	163	DRDGTINSEFQHVISRSPDFASSFKI 189
DB	283	DGDSSINFAEFHVSRSRPFIRTFHI 309

RESULT 2

T41632

probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000

C/Accession: T41632

R/McDougall, R.M.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.
submitted to the EMBL Data Library, August 1999

A/Reference number: Z22005

A/Accession: T41632

A/Status: preliminary; translated from GB/EMBL/DBJ

Query Match 21.9%; Score 210.5; DB 2; Length 174;
Best Local Similarity 27.2%; Pred. No. 2e-09;
Matches 49; Conservative 46; Mismatches 68; Indels 17; Gaps 4;

QY 1 MGSGSRSLKLLAEYODLFLTQLLEILLARRCELLPQQRVYESSLRQAQPEEQLLS 60
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MGQSOSQTEDELIN---SSFSNEETIRIKRRFK-----IDANQSGSIDRNEPLS 48

QY 61 LPELKANFKEKRICRVSTSPAKDSLSEDFEDLDLTLSVDPATPDIKSHVAFRIFPFDD 120
:::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 49 IPSVANPNLARLSVSVDDEGGD-VDEQEELINSLSVSVANGNNEKKRKFKITIDIRD 107

QY 121 GTLNREDLSRYNCLTGEGEDPTRLSASEMKOLINDILESDIDRDGTINLSEFOHVISRS 180
||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 108 GLYSNGELYLVKMMWVG---TNLRDQLQIVDKTIMEVDKDRDKISFEERFDIYVGS 163

RESULT 3

phosphoprotein phosphatase regulatory chain - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: calcineurin chain B homolog; protein phosphatase 2B chain B; protein C/Species: *Saccharomyces cerevisiae*
C/Date: 31-Mar-1992 #sequence.revision 31-Mar-1992 #text.change 20-Jun-2000
A/Accession: JH0462; A45021; S33962; S38022; S34680; S52282
R/Kino: T.; Tanaka, H.; Mukel, H.; Chang, C.D.; Hitzaga, K.; Miyakawa, T.; Tanaka, C.
Biochem. Biophys. Res. Commun. 180, 1159-1163, 1991
A>Title: cDNA cloning of a calcineurin B homolog in *Saccharomyces cerevisiae*.
A/Reference number: JH0462; MOTID:92062059; PMID:1659397
A/Molecule type: mRNA
A/Residues: 1-175 <KUN>
A/Cross-references: EMBL:D10293; NID:g218409; PIDN:BA01136.1; PTD:g218410
R/Cyert, M.S.; Thorner, J.
Mol. Cell. Biol. 12, 3460-3469, 1992
A>Title: Regulatory subunit (CNB1 gene product) of yeast Ca²⁺/calmodulin-dependent phosphatase
A/Reference number: A45021; MOTID:92334345; PMID:1321337
A/Accession: A45021
A/Molecule type: DNA
A/Residues: 1-175 <CYE>
A/Cross-references: EMBL:M87508; NID:g171250; PIDN:AAA34505.1; PTD:g171251
R/Note: sequence extracted from NCBI backbone (NCBIN:108731, NCBIPI:108732)
R/Cheret, G.; Matheakis, L.C.; Sor, F.
Yeast 9, 661-667, 1993
A>Title: DNA sequence analysis of the YCN2 region of chromosome XI in *Saccharomyces cerevisiae*
A/Reference number: S33960; MOTID:93348778; PMID:8394042
A/Accession: S33962
A/Molecule type: DNA
A/Residues: 1-175 <CHE>
A/Cross-references: GB:A69765; NID:g296985; PIDN:CMA49421.1; PID:g296988
A/Experimental source: strain S288C
R/Kleemann, S.; Voss, H.; Schweiger, C.; Rupp, T.; Grothues, D.; Sensen, C.; Stegemann, J.
Submitted to the Protein Sequence Database, March 1994
A/Reference number: S37825
A/Accession: S38022
A/Molecule type: DNA
A/Residues: 1-175 <WIE>
A/Cross-references: EMBL:Z28190; NID:g486336; PIDN:CAA82034.1; PID:g486337; MIPS:YKL190k
A/Experimental source: strain S288C
R/Mela e Silva, A.; Bosser, P.; Vilola, C.; Fernandes, L.; Soares, H.; Guerreiro, P.; R.
Submitted to the Protein Sequence Database, March 1994
A/Reference number: S38024
A/Accession: S38027

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A:Molecule type: DNA
A:Residues: 1-175 <MA1>
A:Cross-references: EMBL:D28190; NID:g486336; PIDN:CAA82034.1; PID:g486337; MIPS:YKL1
A:Experimental source: strain S288C
R:Wiemann, S.; Voss, H.; Schagger, C.; Rupp, T.; Stegmann, J.; Zimmermann, J.; Groth
submitted to the EMBL Data Library, July 1993
A:Description: Sequencing and analysis of 51.5 klobases on the left arm of chromosome
A:Reference number: S34679
A:Accession: S34680
A:Molecule type: DNA
A:Residues: 31-175 <M12>
A:Cross-references: EMBL:X74151; NID:g450365; PIDN:CAA52248.1; PID:g395235
A:Experimental source: strain S288C
R:Pado, J.M.
submitted to the EMBL Data Library, September 1993
A:Description: The protein phosphatase calcineurin is essential for NaCl tolerance in
A:Reference number: S52281
A:Accession: S52282
A:Molecule type: DNA
A:Residues: 1-175 <PAR>
A:Cross-references: EMBL:Z26521; NID:g473144; PIDN:CAA81290.1; PID:g473146
C:Genetics:
A:Gene: SGD:CNB1; YCN2
A:Cross-references: SGD:S0001673; MIPS:YKL190w
A:Map position: 11L
A:Introns: 18/1
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11
F:2-175/Product: phosphoprotein phosphatase regulatory chain #status predicted <MAT>
F:51-52/Domin: calmodulin repeat homology <EF1>
F:53-83/Domin: calmodulin repeat homology <EF2>
F:90-122/Domin: calmodulin repeat homology <EF3>
F:131-163/Domin: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status experimental

Query Match 21.3% Score 204.5; DB 2; Length 175;
Best Local Similarity 27.1% Pred. No. 5.8e-09;
Matches 48; Conservative 44; Mismatches 68; Indels 17; Gaps 4;

OY 1 MGGSSRLSKLLAEYODLTFLTKOELLARRPCELLPOEQRIVESSLRAOVPEQILS 60
Db 1 MGAPSKRYVDLLE---TNFDRDEIRLKRFPKKLDRDSSGSDKN-----EFMS 48
OY 61 LPELKANDFKRIRICVESTSPAKDLSFEDFLDLVSFDPATPDIKSHVAFRLFPDD 120
Db 49 IPGVSSNPLAQRIMEVFADNSGD-VDFQEFITGLSIFSGSKDEKLRFAFKYIDDKD 107
OY 121 GTINREDLSRVNCLTGEGEDTSLASAMKOLLINLEESDIDRGTINTLSEFQAVI 177
Db 108 GFISNGELFVLKIMVG---SNLDEQLQIQIVRTIYENDSGDGRSLSEFEKMAI 160

RESULT 4
T47245
calcineurin regulatory chain [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
C:Accession: T47245
R:Dieminger, M.; Troppschug, M.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z24421
A:Accession: T47245
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-174 <DIE>
A:Cross-references: EMBL:Y12814; PIDN:CAA73345.1
A:Experimental source: strain 74 A
C:Genetics:
A:Gene: Can B
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand

Query Match 20.7% Score 199.5; DB 2; Length 174;

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```
Best local Similarity 26.1%; Pred No. 1.4e-08;
Matches 41; Conservative 42; Mismatches 61; Indels 13; Gaps 3;

OY      24 KQETLLAHRFCCELLDQEORTVESSLRQAQPPEQLSLPBLKAMPFKRICRFVSPAK 83
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      20 REEVRLRRFRFMKLKDNGSTIER-----EEFLSQISTNPPLATMAIFDNCGG 71

OY      84 DLSLSEDFDLDSVESDTLPDIKSHPAFRIEDFDGGTLNRNDSLRYNLCTGEDETR 143
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      72 D-VDFEELFVSGLSAFSRKGNKEOKLFPAKFYVDIDRGGISNGELFYLVKMVG----SN 126

OY      144 LSASEMKOLINDLESDDIDROGTINLSEFOHYSRS 180
       |::::::::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      127 LMDQQLRVIVDKTIMERADLDKGKISFEFTKMENT 163

RESULT 5
A33391
calcinurin regulatory chain - human
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase C; Species: Homo sapiens (man)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Jul-1999
C:Accession: A33391
R:Guertin, D.; Krinks, M.H.; Sikela, J.M.; Hahn, W.E.; Klee, C.B.
DNA 8, 675-682, 1989
A:title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-binding protein from sheep brain
A:Reference number: A33391; NCBI:90126237; PMID:255868
A:Molecule type: mRNA
A:Residues: 1-170 <GUE>
A:Cross-references: GB:M30773; NID:g180704; PID:NAB08721.1; PID:g180705
C:Genetics:
A:Gene: GDB:P393R1; CALNB
A:Cross-references: GDB:I36804; OMIM:601302
A:Map position: 2p16-p215
C:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin repeat homology <EF1>
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11pop F-18-49/Dominant: calmodulin repeat homology <EF1>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2-Modified site: myristylated amino end (Gly) (In mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted
F:31/33/35/37/42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted
F:63/65/67/69/74/Binding site: calcium (Asp, Asn, Glu, Glu) #status predicted
F:100/102/104/106/111/Binding site: calcium (Asp, Asp, Tyr, Glu) #status predicted
F:141/143/145/147/152/Binding site: calcium (Asp, Asp, Arg, Glu) #status predicted

Query Match          19.4% Score 186.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.4e-07;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

OY      56 EQLSLPELKMPFERICRFVSPAPSDSLEDFDLDSVESDTATPDIKSHYAERI 115
       |:|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      41 EEPSMLPELQNPLPVORVIDLFSTD-GNGEYDFKEIEFGVASOFVKGDKEOKLFFAEFIY 99

OY      116 DEEDDTLNREDLSRTYNCLTGEGEDTRLASAMKKOLIDNTLESDDIDROGTINLSEQH 175
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      100 DMNDKGYISNELPYVLKMVG-----NNLKTFQIQIYDKITINNADKDGGRIRISFEERCA 155

OY      176 VI 177
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      156 VV 157

RESULT 6
S34127
calcinurin regulatory chain [validated] - bovine
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase C; Species: Bos primigenius taurus (cattle)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000
```

C:\Accession: I45831; J0297; S34127
R:Nargang, C.E.; Bottoriff, D.A.; Adachi, K.
DNA Seq. 4, 313-318, 1994
A>Title: Isolation and characterization of a cDNA clone coding for the calcium-bind
A:Reference number: I45831; MUID:95102111; PMID:7603816
A:Accession: I45831
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-170 <NA2>
A:Cross-references: EMBL:X71666; NID:g312968; PIDN:CAAS0659.1; PID:g312969
R:Altken, A.; Klee, C.B.; Cohen, P.
Eur. J. Biochem. 139, 663-671, 1984
A>Title: The structure of the B subunit of calneurin.
A:Reference number: J0297; MUID:84132092; PMID:6521184
A:Accession: J0297
A:Molecule type: protein
A:Residues: 2-11; 'M', 13-153, 'S', 155-169 <AIT>
R:Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sittachak, M.D.; Thomson, J.A.; Fitzgibbon, J.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A66708; PDB:1TGO
A:Contents: annotation: X-ray crystallography, 2.5 angstroms, residues 2-170
R:Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sittachak, M.D.; Thomson, J.A.; Fitzgibbon, J.
Cell 82, 507-522, 1995
A>Title: X-ray structure of calneurin inhibited by the immunophilin-immunosuppres-
A:Reference number: A59667; MUID:95360994; PMID:7543369
A:Contents: annotation: X-ray crystallography, 2.5 angstroms
A:Complex: heterodimer with calneurin catalytic chain (see PIR:A56968)
C:Superfamily: calmodulin, calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer;
F:2-170/Product: calneurin regulatory chain #status experimental <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status experiment.
F:3/Modified site: aspartic acid (Asn) #status predicted
F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status experiment.
F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asp, Glu, Glu) #status experiment.
F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status exper
F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status exper

Query Match 19.4%; Score 186.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.4e-07;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPFERIGRVSTSPAKDSLSEDFDLILVSFDTATPDIKSHVAFRIP 115
DB 41 EEFMSLPKELQNPILVORVIDIDPTD-GNGEYVFKKEFIEGVSQPSVKGDKQKLRFAFRIR 99
QY 116 DFDGGTGNREDLSLVNCLTGEDETRLSADEMKOLLINLEESIDIDNGTINLSEFOH 175
DB 100 DMDKRDGYISNGELFOVLKMAVG---NNLKDTQLOQIVDKTITINADKDGGRISFEFCA 155
QY 176 VI 177
DB 156 VV 157

RESULT 7
JC1220
calcineurin regulatory chain, brain - mouse
N:Alternate names: calcineurin beta-1 subunit; calcineurin chain B-1; phosphoprotein.
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JC1220
R:Ueki, K.; Muramatsu, T.; Kincaid, R.L.
Biochem. Biophys. Res. Commun. 187, 537-543, 1992
A>Title: Structure and expression of two isoforms of the murine calmodulin-dependent
A:Reference number: JC1220; MUID:92392379; PMID:1325794
A:Accession: JC1220
A:Molecule type: mRNA
A:Residues: 1-170 <DEK>
A:Cross-references: GB:S43864; NID:g255078; PIDN:AA23171.1; PID:g255079

QY 35 CELLP0EO-----RTVSSSLAQPVEQIISLPKANKPFRICRVFTSPARDSL 86
 Db 12 CNHDOBEIRRLGRKSPFKRLDLDKSGSLSEFEMRLPELQNPVLGVRVIDFTD-GNGEV 70
 QY 87 SEFEFLLLSVSPDTPARPDIKSHYAFIPDDGTLNREDSLVNCLTGESEDTRSA 146
 Db 71 DHEEFTVGTSGFVKGEDEQKLRFAFRIDMDNDGFIISGELFQVLYKMWG---NNLKID 126
 QY 147 SEMKOLIDNILESDIDRDGTINLSEFOHY 177
 Db 127 WQLQQLVYDKSLVLDKDGGRISFEERSDVY 157

RESULT 14

PS0261
 calmodulin regulatory chain-11k protein, testis - rat (fragment)
 N:Alternate names: calmodulin beta subunit; calmodulin chain B; phosphoprotein phosphatase
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Mar-1992 #sequence, revision 31-Mar-1992 #text, change 13-Aug-1999
 C/Accession: PS0261
 R/Sugimoto, M.; Matsui, H.; Etch, S.; Shimizu, T.; Nishio, H.; Mota, L.J.M.P.; Tokuda, M.
 Blochem. Biophys. Res. Commun. 180, 1476-1482, 1991
 A>Title: Isolation and sequence of rat testis cDNA for a calcium binding polypeptide sim
 A/Reference number: PS0261; M0ID:92062183; PMID:1659420
 A/Accession: PS0261
 A/Molecule type: mRNA
 A/Residues: 1-165 <SUG>
 A/Cross-references: GB:S63991; NID:9238643; PIDN:AAB20281.1; PID:9238644
 C/Superfamily: calmodulin; calmodulin repeat homology
 C/Keywords: blocked amino end; calcium binding; duplication; EF hand
 F:/38/Domain: calmodulin repeat homology <EF1>
 F:/39-71/Domain: calmodulin repeat homology <EF2>
 F:/76-108/Domain: calmodulin repeat homology <EF3>
 F:/117-149/Domain: calmodulin repeat homology <EF4>

Query Match 17.7%; Score 170.5; DB 2; Length 165;
 Best Local Similarity 31.1%; Pred. No. 2.3e-06;
 Matches 38; Conservative 28; Mismatches 51; Indels 5; Gaps 2;

QY 56 EQILSLPELKNPFRICRVFTSPAKDSLSEFEDLDSVSPDTPARPDIKSHYAFRI 115
 Db 30 DERMSLELQNPVLGVRVIDFTD-GNGEVDFREFIVGTSGFVKGEDEQKLRFAFRIT 88
 QY 116 DFDDGTLNREDSRLVNCITLGESEDTRLSASEMKOLIDNILESDIDRDGTINLSEFOH 175
 Db 89 DMDNDGFIISGELFQVLYKMWG---NNLKMDQLQQLVYDKSLVLDKDGGRISFEERSD 144
 QY 176 VI 177
 Db 145 VV 146

RESULT 15

QY1232
 calmodulin regulatory chain-11k protein - rat
 N:Alternate names: calmodulin chain B-like protein
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Mar-1992 #sequence, revision 31-Mar-1992 #text, change 20-Jun-2000
 C/Accession: QY1232
 R/Mukai, H.; Chang, C.D.; Tanaka, H.; Ito, A.; Kuno, T.; Tanaka, C.
 Biochem. Biophys. Res. Commun. 179, 1325-1330, 1991
 A>Title: cDNA cloning of a novel testis-specific calmodulin B-like protein.
 A/Reference number: QY1232; M0ID:92028870; PMID:1718268
 A/Accession: QY1232
 A/Molecule type: mRNA
 A/Residues: 1-176 <MUK>
 A/Cross-references: GB:D10393; GB:D90449; NID:9220687; PIDN:BA01232.1; PID:9220688
 A/Experimental source: testis
 A/Note: this protein appears to be expressed specifically in testis
 C/Superfamily: calmodulin; calmodulin repeat homology
 C/Keywords: blocked amino end; calcium binding; duplication; EF hand; lipoprotein; myristic
 F:/16/Product: calmodulin regulatory chain-like protein #status predicted <MUK>
 F:/18-49/Domain: calmodulin repeat homology <EF1>

F:/50-82/Domain: calmodulin repeat homology <EF2>
 F:/87-119/Domain: calmodulin repeat homology <EF3>
 F:/128-160/Domain: calmodulin repeat homology <EF4>
 F:/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:/3/Modified site: aspartic acid (Asn) #status predicted

Query Match 17.7%; Score 170.5; DB 2; Length 176;
 Best Local Similarity 31.1%; Pred. No. 2.5e-06;
 Matches 38; Conservative 28; Mismatches 51; Indels 5; Gaps 2;

QY 56 EQILSLPELKNPFRICRVFTSPAKDSLSEFEDLDSVSPDTPARPDIKSHYAFRI 115
 Db 41 DERMSLELQNPVLGVRVIDFTD-GNGEVDFREFIVGTSGFVKGEDEQKLRFAFRIT 99
 QY 116 DFDDGTLNREDSRLVNCITLGESEDTRLSASEMKOLIDNILESDIDRDGTINLSEFOH 175
 Db 100 DMDNDGFIISGELFQVLYKMWG---NNLKMDQLQQLVYDKSLVLDKDGGRISFEERSD 155
 QY 176 VI 177
 Db 156 VV 157

Search completed: November 21, 2002, 18:00:18
 Job time: 18 secs